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Query Match
Best Local Similarity
Matches 1527; Conserv
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AX469820 Sequence
AP005282 Corynebac
BX927155 Corynebac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AXI27152 Sequence
AXI22988 Sequence
BD165105 Novel pol
BD092238 DNA encod
AX069136 Sequence
AL93252 Lattobaci
132039 Pediococous
Z32771 P.pentosace
AF401046 Lattobaci
Z97015 Lactococcus
AF01511 Streptococ
AE015011 Streptococ
AE017019 Lactobaci
                                                                                                            October 30, 2004, 12:45:36; Search time 6341 Seconds (without alignments) 11388.010 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                               1 ctcatggcatctgcgccgtt.....gttgaaaccttgagtgttcg 1527
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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BD093238
AX069136
AL935252
PDCRAFOPER
                                                                       nucleic search, using sw model
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Maximum Match 100%
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Gaps

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ilarity 100.0%; Score 1527; Conservative 0; Mismatches

Length 1527; Indels

09 1081 CATCTTTGCCAGCGGAAAGCTTCGCGCGGAAAGCTTCGCGCGGGAAAGCTTCGCCGGGGAAAGCTTCGCCGGGGAAAGCTTCGGCTGGGAAAGATTGTGGTGTGTGT	7
1 CTCMTGGCATCTCCCCCTTCCCCATCTCTCCCATGTTTGGTTTGTTT	
8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6	v

KGTADFLITPVLTLLTCELTFIALGPARRWYGDVLAHG
YSPILVTUTGLGOFPATELELNOGGSPIFATASMANIAO
AGASGWSAVIGITEPAIGCONNELRWEFFIFATASMANIAO
GVUSIDAPDWWFLVCAVVTFFIAFGAALAYGUTAALGG
GVUSIDAPDWTGTIQAPLTGEAIALSSVSDAMFASGKL
KRIVVAPPSSGHAFNYTKABOGSWDIIMHIGPOTVNING
CGFDIDAIKAAGYBVTTPIVVSNYKKTGPVNTYGLGIG 1140 1380 1200 1260 1320 1320 PAT 09-AUG-2002 1200 BATGCCATTAAGGCTGCAGGTTATCAGGTAAC 1380 AAAACCGGACCTGTAAACACTTACGGTTTGGG 1440 AAAACCGGACCTGTAAACACTTACGGTTTGGG 1440 ACGTCGCAAAGAAAGAAGCGGTGCCAGCAAC 1500 ACGTCGCAAAGAAGAAGCGGTGCCAGCAAC 1500 GGGTTGCCATCGTCCCAAGGGGCAGTT cecreaagaagcaggccarcaagcc TGGCATTCCCATCTGGCCATGCTTTCGCAGT TEGATATCTTGATECACATTGGTTTCGACAC CGCTGAAGAAGCAGGGCGATGAAGTCAAAGC nobacteridae; Actinomycetales; riaceae; Corynebacterium. r, O. and Schroeder, H. n product; RXS00315" linear erium glutamicum" DNA" DNA -2002; 1527 1527 231.

1527; DB 6; Length 1527; vo. 0;

gene

CDS

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VIALLI FPLILAAALOYLYDRKLGGHLYDPANGGSILMQHLFWFFGHPEVYVLALPFF
GIVSELI PVFSRKEMFGYVGLI FATLS I GALSMAVWAHMFYTGAVLLPFFSFWTFL
GSVPGYKFFRWYGTWWGTHTWETPMI WSYGFMATFLFGGGLTGTMLASPPLDFHLADS
YFLIAHFHYTLFGTVVFASCAGVYFWFPKMTGRMDERLGKIHFWLTFVGFHGTFLIQ
HWYGNMGMPRRYADYLSDGFTI YNQI STVPSFLIGLSVI PPI UNVPKSWRYGELYYV
DDPWGYGNSLEWATSCPPPRHNFASLPRI RSERPAFELHYPHMI ERWRABAHTGHHDD
I NAPELGTAPALASDSSR"
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FANYVLPLQIGAPDVAFPRLNAFGFWITTVGGVAMLTGFLTPGGAADFGWTWYSPLSD
AIHSPGLGSDNWIVGVGATGIGSVASAINMLTTILCLRAPGWTWFRNPIFTWNIFVVS
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PTVNPCHRFHNSPRRGSIEWLRRPFQGRFLLKRDVPPRGPRGAMRSPTPICASEKPAP
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GLLRRSKRLVCPDCDSTLITGEVIEKLAAHAGKEARVAAVTERAMRGELDFEESIKER
VKALAGLDASVI DEVAAALIELTPGARTITRTINRMGYQTAVVEGGFIQVLEGLBEELE
LIDYRANTLEI VDGALTGNYTGKI VDRAAKABFIREFABSGGLKMYQTVAVGGANDI
DMLSAAGLGVAFNAKPALKEI ADTSVNHPFLDEVLHIMGISRDEIDLADQEDGTFHRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="PF00115;Cytochrome C and Quinol oxidase polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
/product="Heme/copper-type cytochrome/quinol oxidases,
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/gene="Cg12525"
/note="PF00268:Ribonucleotide reductase, small chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /EC_number="3.1.3.3"
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/InGReo.099:TIGRO0099: conserved hypothetical protein
TIGRO0338:serB: phosphoserine phosphatase SerB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/transl_table=1.1
/product="Phosphoserine_phosphatase"
/protein_id="RAB9915.1"
/db_xref="G1:21325294"
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db xref="G1:21325296"
                                                              /trans] table=11
/product="Uncharacterized ACR"
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/gene="Cg12523"
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                                       codon start=1
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Thasfyesiakaipilsilltilvtvngissgnpvqppaleqvrtdvvnkinyernlk
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YREGEI Y PPOSPLIJVRGTFABCVI LETVI ILS IMNADSAVASAAARMYTAADGRPI I B
MGSRRTHEY SAVTASRAAYLAGFSTTSNLEAAYRYGI PASGTSAHAMTLLHINDDGTP
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KOLDDLAHNTKILVUSSDLDEFAIAGLRGBPPVDVGVGVGTVTGSGPPAGLVYKIV
EVAGHPVAKRSRNKESYGGGKKAVRTHKKGGTAIEETVYFFNAEAPDTGKLJTLSLTI
PLARDGEIVPLESSRAYIAKQLVSLPWEGIALSRDEPVLHTRFVGFPPAA"
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QVSVTARECIGASRCPHGEDCFAEIARGKAKEADVVVTNHALLAIDALSDVSVLPEHD
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TMQPGRWNDMDEGSKGTLVALKDALWALRAQIAGAPEGEAANDPERFAERQNLSNHLM
EIHDANVRILEVFAEEDPSKQYDVVWHNHDDRRGDSLNVAPLSVAGLLHEKLFAENTV
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BETLDDET YELLTAAGGRTLGLFSSKRAABQAPTKAMRLALPFDVLCGDDNTAALVKK
FSDSENTCLFGTLITHQGVDVPGRSLSLULLDRI PFPREDDPLLQARKRAADAGGRNG
FSDSENTCLFGTLITHQGVDVPGRSLSLULLDRI PFPREDDPLLQARKRAADAGGRNG
FMEVAATHAALLMAQGAGRLLRHVGDRGVVAVLDHRLSTKRYGGFLRFSMPRFWETTN
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PFDQGFNaYSSPIPPEVPQPSMQBAQWRSFDLGTVFGQAWKGFTATWQAWVLSALIYF
AVLLVLMFAWILFMVSVLAATSSGSDSAAIAATGGTSFFGFMLMIVLAFISFVYSLNC
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AVPVAFQLRDASIGDAFSASWKAVSKNVGQVILLELAIFALSFLGSAVIIGMLVTTPL
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protein_id="BAR99913.1"
db_xref="GI:21325292"
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complement (5587. .6312)
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Corynebacterium glutamicum ATCC 13032
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
(Dases 1 to 349136)
Kalinowski,J., Bathe,B., Bartels,D., Bischoff,N., Bott,M.,
Burkovski,A., Dusch,M., Huthmacher,K., Kramer,R., Inke,B.,
Goesmann,A., Hartmann,M., Huthmacher,K., Kramer,R., Linke,B.,
Rey,D.A., Ruckert,C., Rupp,O., Sahm,H., Wendisch,V.F., Wiegrabe,I.
and Tauch,A.
                            147298 GGCAGTTGCGTTGCGCTGCAGGTTTCTTGGTTGTTTCTTTGATGCTCCAGATAT
                                                                                                  147238 GGTCATGTTCTTGGTGTGCAGTTGTTACTTTCTTCATCGCATTCGCAGCGAGTGC
                                                                                                                                                                          TTATGGCCTTTACTTGGTTCGCCGCAACGCAGCATGATCATCATGCAGATGCAACGCTGCTCC
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                                                                                                                                                                                                                                                        147118 AGTECCTECAGGAACGACCAAAGCCGAAAGCAGAAGCACCCGCAGAATTTTCAAACGATTC
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                                                                                                                                                                                                                                                                                                                                                                        146998 CARGITIGCCAGCGGAAAGCTIGGCTCGGGCGTIGCCATCGTCCCAACCAAGGGGCAGTT
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Corynebacterium glutamicum ATCC
complete genome; segment 8/10.
BX927155 BX927147
BX927155.1 GI:41326514
                                                                             GGTCATGTTCTTGGTGTGTGTGCAGT
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DEFINITION
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VERSION
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LNNLGYEGLFPADETKVSPNILLSALSPNADENHDFFSGSGSSYVIGKAENTEDDDWDF
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Pred. No. 0;
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/gene="Cg12526"
11555. .12043
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SNTFIVYSIVSSTSIRALFRAGVGPCLLMILACVIVGTWLARKENYKREQHEPTRQS
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(PERMEASE LARGE PROTEIN)"
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NLTILIAIPFALVLIVMAIAFIKDLSTDPAAIRQRYAKAAISNAVVRGLEEHGDDFEL
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complete Corynebacterium glutamicum ATCC 13032 genome sequence its impact on the production of L-aspartate-derived amino acids
                                                                                                                                                                                                                                                   Submitted (21-37N-2004) Joern Kalinowski, Institut fuer Genomforschung, Universitaet Bielefeld; Universitaetsstrasse 25, 33615 Bielefeld, Germany
Be-mail:Joern KalinowskiaGebitec.Uni-Bielefeld.DE
This sequence was accomplished by collaboration between Degussa AG and Bielefeld University.
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BX927150.1:51. .348459, BX927152.1:51. .349799, BX927153.1:51. .349558
BX927154.1:51. .349575, BX927155.1:51. .349136, BX927156.1:51. .3491186.
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complement (67. .729)
                                                                               J. Biotechnol. 104 (1-3), 5-25 (2003) 22830012
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RESULT 5 AX127152 LOCUS DEFINITION Sequence 7068 from Patent EP1108790. AX127152 AX121152 AX127152 AX114121 VERSION SEQUENCE OCTYNEBACTERIUM Glutamicum COTYNEBACTERIUM Glutamicum ORGANISM BACTERIUM COTYNEBACTERIUM Glutamicum COTYNEBACTERIUM Glutamicum BACTERIUM COTYNEBACTERIUM Glutamicum COTYNEBACTERIUM Glutamicum BACTERIUM COTYNEBACTERIUM Glutamicum COTYNEBACTERIUM COTYNEBACTERIUM AUTHORS VOKO1, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A. TITLE AUTHORS VOKO1, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A. TITLE AUTHORS JOURNAL COTYNEBACTERIUM COTYNEBACTERIUM COTYNEBACTERIUM COTYNEBACTERIUM AND HAKKO KOGYO CO., LID. COTYNEBACTER	Duery Match 99.2%; Score 1515; DB 6; Length 349980; Best Local Similarity 99.9%; Pred. No. 0; Matches 1526; Conservative 1 CTGTGGGCGTTCGCGGTTCTGGCGTGTTGGTTGGTTTCACCGCAACCAAG 1111326 CTCATGGCCGTTCGGGTTCTTGGCTGTTGGTTTCACTGGAACCAAG 111266 CTCATGGCGAATGAGTTCCTGGGCGCGGTATTGGTTTGGTTTCACCGCAACCAAG 111266 CGTTTCGGCGCAATGAGTTCCTGGGCGCGGTATTGGTATGGTTTCACCGCAACCAAG 111266 CGTTTCGGCGCAATGAGTTCCTGGGCGCGGTATTGGTATGGTATTGGTTTCCCGAG 111267 CTTGGTGAACGGCTACCAGGCGCGCGGTATTGGTATGGTATTGGTATTCCCGAG 111127 CTTGGTGAACGGCTACGAGCGCGCCACCATGGCGGCACCAATGTGGTC 111147 CTTGGTGAACGGCTACGACGGCGCCCACCATGGCGGCACCATGTGGTC 111147 CCTGTTTGGATTTCGGCAACCAGGCGCCCACCGGCGAATGCCATGTGGTC 111168 CTTTCTTGGATTCTGGCAACGGGCACCAGGCACCGTGCTTCCTGGTC 111087 GGTTTCTTGGATTCTGGCAACGGGTACCAGGGCACCGGCACCTGGTTCTGGTC 301 AGACTTCCTGGATCGCCAACGGGTTACCAGGGCACCGGCACCTGGTTACATGTGGTC 111087 GGTTTCTTGGATTCTGGCAACGGGTTACCAGGGCACCGGCACTGGTTACATGTGGTC 111087 GGTTTCTTGGATTCTGGCAACGGGTTACCAGGGCACCGGCACCTGGTTACATGTGGTC 111087 GGTTTCTTGGATTCTGGCAACGGGTTACCTGCTCACAGGGCACTGGTTACATTCATCGC 301 AGACTTCCTGGATCGACGGGTCGACGGGTTACCTGCACAAGCGACTTCATACATTCATCGC 301 AGACTTCCTGGATCGACGGGTCGACGGTTCCTGCTCACAGGGCACTTCATACAGTTCATCATCATCATCATCATCATCATCATCATCATCATCA	Db 110907 TGATTTCGGTGGTCGGCGGTCTTCGGTCTGGTCTACTCACCAATGGTCAT 110848 Qy 481 CACTGGTCTGCACCAGTCCTTCCCGCCAATTGACTGGTCTTTAACCAGGGTGGATC Db 110847 CACTGGTCTGCACCAGTCCTTCCCGCCAATTGACTGGACTGTTTAACCAGGTGGATC Qy 541 CTTCATCTTCGCAACGGCATCTATGGCTAATATCGCCCAGGGTGCAGTTTGGCAGT Db 110787 CTTCATCTTCGCAACGGCATCTATGGCTAATATCGCCCAGGGTGCGATGTTTGGCAGT Oy 601 GTTCATCTTCGCAACGGCATCTATGGCTAATATCGCCCAGGGTGCGATGTTTGGCAGT Oy 601 GTTCATCTTCGCAACGGCATCTATGGCTAATATCGCCCAGGGTGCTGTTTGGCAGT III0787 CTTCATCTTCGCAACGGCATCTATGGCTAATATCGCCCAGGGTGCTGCTTTGGCAGT III0787 CTTCATCTTCGCAACGGCATCTATGGCTAATATCGCCCAGGGTGCTTTGGCAGT III0787 CTTCATCTTCGCAACGGCATCTATGGCTAATATCGCCCAGGTGCTTCTCGCCGCT IIIIIIIIIIIIIIIIIIIIII

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JP 2002191370-A/2904
09-JUL-2002
15-DEC-2000 JP 2000405096
SATOSHI NAKAGAWA, HIROSHI MIZOGUCHI, SEIKO ANDO, MIKIO HAYASHI, KEIKO OCHIAI,
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AUTHORS Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K.,
TITLE Novel polynucleotide
JOURNAL Patent: JP 2002191370-A 2904 09-JUL-2002;
KYOWA HAKKO KOGYO CO LTD
WMENT OS COTYNEBACTERIUM glutamicum
PN JP 2002191370-A/2904
PP 15-DEC-2000 JP "
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Corynebacterineae; Corynebacteriaceae; Corynebacterium
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Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai
Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A.
Novel polymucleotides
Patent: EP 1108790-A 2904 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)
Location/Qualifiers

    1983
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/mol type="unassigned DNA"
    /db_xref="taxon:1718"

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Izui,M., Sugimoto,M., Nakamatsu,T. and Kurahashi,O.
DIAM encoding sucrose PTS enzyme II
Patent: WO 0102584-A 11-JAN-2001;
AJINOMOTO CO INC,MASAKO IZUI,MASAKAZU SUGIMOTO,TSUYOSHI NAKAMATSU,
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G01N33/56,

PC G1N33/56,

PC (G12N1/21, C12R1:13), (C12N1/21, C12R1:01), (C12P13/08, C12R1:15),

PC C12N15/00, C12N15/00

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COMMENT OS Brevibacterium lactofermentum PN WO 0102584-A/1 PD 11JAN-2001 PF 30-JUN-2000 WO 2000JP004348 PR 02-JUL-1999 JP 99P 189512 PI NASAKO IZUI,MASAKAZU SUGIMOTO, TSUYOSHI NAKAMATSU, OSAMU PI KIRAHASHI PC C12N15/54, C12N9/12	FEATURES FT CDS Location/Qualifiers FEATURES 1.5969 (3779). (5761). Source 1.5969 (00000000000000000000000000000000000	Y Match Local Similarity 95.7%; Score 1412.6; DB 6; Length 5969; Local Similarity 95.7%; Pred. No. 0; hes 1462; Conservative 0; Mismatches 64; Indels 1; Gaps 1 CTCATGGCATCTGGCGTTCGGCGTTCTGCCAGTGTTGGTTTCACCGCAACCAAG	61 CGTTTCGCGCCAATGAGTTCCTGGGGCGCGTATTGGTATGGCGATGGTGTTCCCGAGG 61 CGTTTCGCGGCCAATGAGTTCCTGGGCGCGCGTATTGGTATGGCGATGGTGTTCCCGAG 6319 CGTTTCGTGAATGAGTTCCTGGGCGCGCG-GCATTGGTATGGCGATGGTGTTCCCCAAC 121 CTTGGTGAACGGCTACGACGTGGCCGCCACCATGGCTGCGGGCGAATGCCAATGTGGTC 6378 CTTGGTGAACGGCTACGACGTGGCCGCCACCATGGCTGGC	181 CCTGTTTGGTTTAGATGTTGCCCAGCGGTTACCAGGGCACGAAAIGCCAAIGTGGTC 4 1840 CCTGTTTGGTTTTGCTTCCCAGGCCGGTTACCAGGGCACCGTGCTTGTTGTTGTTGTTTGCTCTAGCTGTTTACCAGGGCACCGTGCTTCCTGTGCTTGTTTGT	301 AGACTICCIGATOCTCACTGCTGACGTTGCTGCTCACCGGATTCCTTACGTCTCTCGC 4558 AGACTTCCTGATCATCCTGCTGCTGCTGCTGCTCACCGGATTCCTTACGTTCATCGC 4558 AGACTTCCTGATCACCCGTGCTGGTGCTGCTGCTCACCGGTTCCTTACGTTCATTGC 361 CATTGGCCCTGGATGCTGGTGGTGGCTGCTGCTGCTCTTACGTTCATTGC 4618 TATTGGTCCAGTGGCTGGGTGGCTGGTGTCTTCGTTTTACTCTTTACTCTTTGGTCTGGTGGTGGTGGTTTTACTCTTTGGTCTGGTGGTGGTTTTACTCTTTGGTCTGGTGGTTTTACTCTGGTGGTGGTTTTACTTTTGGTTCTACTGGTGGTGGTCTTTTGGTTCTTTTTGTTCTGGTTGGT	481 4738 541 4798 601 4858 661 4918

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Proc. Natl. Acad. Sci. U.S.A. 100 (4), 1990-1995 (2003)
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Kleerebezem,M. and Siezen,R.J.
Direct Submission
Submitted (14-0CT-2002) Wageningen Centre for
Box 557, 6700 AN Wageningen, The Netherlands
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="WCFS1"
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NNYGGLGBIRAGANLANYAKKAAVPATP"
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0; Mismatches 1;
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IPRQIAMYLSRELTESSLPRIGNEFGCKDHTTVIHAHDKITKALKTDAELQKAVGDLT
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VGLGKTHLMHAIGNKLLETDPTSNIKYVTSESFTNELINAIOTKKOEAFREBYRNVDL
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PDQWIKLERNOVLFVLGOTSPYSRLLEGONYPDTSKLIPKERSNITVEISARALSRA
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db xref="TrBMBL:Q890K6"
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db_xref="TrEMBL:Q890K5"
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3444. .4568
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/gene="recF"
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gene

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CDS

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SKARVAAKRAREVTRKKSGLEISNLPGKLADNSSKDPEISELFIVEGDSAGGSAKQGR
                                                                                                                                                                                                                                                                                                                                                                                                                                         SRLTQAILPIRGKIINVEKASIDKILANEEIRSLFTAMGTGFGGDFDLSKANYHKLII
MTDADVDGAHIRTLLLFLFYRYMRPLVDAGFVYIAQPPLYQVRQGKFVKXIDSDEELS
EVMGQLAPSPKPVVQRYKGLGEMDAEQLMETTMDPDKRRLLRVRDEDAADADGVFSML
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                                                                                                                                                                                                KTPMKI IGDAPDDAHGTAVHFVPDPDI FRETTTYDINI LITRIRELAFINKGLRITIR
DNRPDEPTEDDFLYEGGIRHYVEYLDKWKTVLFPEPII YVGGEQNGITVEVALQYTDDY
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TVYTILHAGGKFGGGGYKVSGGLHGVGASVVNALSSTLDVKVTRNGHVYYNDFERGKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DWSKRRFAYEIGGFNEGTYHIVNLTATDDAALNEFDRLSKINDDILRHMIVKRED"
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protein id="CAD62710.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'product="ribosomal protein S6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGDQVKPRREFIEDNAKFVQDL.DV"
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6676. .9237
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trans1_table=
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'transl table=
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'gene="ssb"
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/gene="rpsF"
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Leathouts, K.J., Bolhuis, A.A., Kok, J.J. and Venema, G.G.
The sucrose and raffinose operons of Pediococcus pentosaceus PPE1.0
The sucrose and raffinose operons of Pediococcus pentosaceus PPE1.0
Unpublished (1994)
On May 25, 1994 this sequence version replaced gi:475106.
Original source text: Pediococcus pentosaceus (strain PPE1.0) DNA;
Insertion sequence IS30 homolog (transposable element Insertion
sequence IS30 homolog, kingdom Prokaryotae) DNA; Pediococcus
pentosaceus (strain PPE1.0) DNA; Insertion sequence IS3 homolog
(transposable element Insertion sequence IS3 homolog
(transposable element Insertion sequence IS3 homolog
Prokaryotae) DNA; and Pediococcus pentosaceus (strain PPE1.0) DNA.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="wingerktlankspesnvlpfoqgeaclpnytykonnvrdsyvihy
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OKLLIKLRLEDAKQRLSTSNNSVQSIANNVGYKDSFTFSKAFKRXSGASPSYYRKSIG
                                                                                                                                                                                                                                                                                                         BCT 23-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       permease; rafP
                                                                                                                                                                                                                                                                                                                                                                                                                                        agak gene; agas gene; agl gene; alpha-galactosidase;
alpha-glucosidase; fructokinase; insertion element; permease; rafi
gene; raff gene; raffinose operon; regulatory protein; scrA gene;
scrB gene; scrK gene; scrR gene; sucrase; sucrose-6-phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pediococcus pentosaceus
Pediococcus pentosaceus
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                        Pediococcus pentosaceus raffinose operon genes.
L32093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pentosaceus"
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/strain="PPB1.0"
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487...510
/note="nRR; putative"
/rpt_type=direct
488...561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (2929. .3864)
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'note="IR1; putative"
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/gene="rafk"
3909. .5918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           table=11
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/trans1_table=
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                                                                                                                                                                                                                                                                                                                                                                                                               L32093.1 GI:493181
                                                                                                                                        AACTTTTATCTATGCC
                                                                         AGCGATTGCTTATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transport protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16532 CACGACTGGTTGGATTGGCATGGGCATCTTTGGCCTTCTCTACTCGGCCATTGTCATTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---AACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166232 ATTTCCATTTGTCTTTGCAGCGATTGCCTCAGGAATTGCTTCAGGTTTGTTAGGACTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424 TTTCGGTGGTCCAGTCGGCGGTCTGCTCTTCGGTCTGGTCTACTCACCAATCGTCATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166352 Triradcrafirircriraccactáadadccaáaadcaaaaadccigacricrircadccd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAATATCAAGGCAGTTGCGTTGGGCGCTGCAGGTTTCTTGGGTGTTTCTATTGATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCAGATATGGTCATGTTCTTGGTGTGTGCAGTTGTTACCTTCTTCATCGCATTCGGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TICGGCGCCAATGAGTICCTGGGCGCCGCGTATIGGTATGGCGATGGTGTTCCCGAGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTCCTGATCACTCCAGTGCTGACGTTGCTGCTCACCGGGATTCCTTACATTCATCGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364 TGGCCCAGCAATGCGCTGGGTGGGCGATGTGCTGCCACACACGGTCTACAGGGACTTTATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                            Length 343050;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                               Score 308.4; DB 1;
Pred. No. 1.4e-71;
0; Mismatches 351;
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/protein_id="CAD62711.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      locus_tag="lp_0011"
       .11073
                                                                                                         .11073
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                                                                                                                                        gene="rpsR"
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                                                                                                            .0837
                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                | gene="agas"
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                                                                                                                                                                                                      TDVNEAAYGESMIGIAKDVPNSIYMTIGTGVGAGYISQNHIFNGRTHTELGHMELNRL.
PGDDFKSNCPYHDICLEGLAAGPAVGKRTGKAGKDIPVDDPVWPIITDYIAQACVNLT
VAFAPDKIILNGGVMNQRQLFPMIREKFAAYLNGYEEVPPLDDYIVPAGLGNNSGIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TILRHHGTTNILQVTALSSAQIDI.PTDQYTALTILSGTRAHEANPS FNRIHPGLOTVRSI.
RGTSGPQHQPFWALAEPNTTELAGTVIGCALAWSGNFDSTVEVDQYQHSRLTIGLEPD
TFWQLKPNSSFQTPEAVLYWTNICFNGMSOVFHDESYQLMESQTNIPSYLAWBTILT
FWASSKYQHLI BHAHGLOLMLYLDDGWFVNRNGENGQLGDWFVDPIKFPNGLNPLA
QQAHHHMKCLWWEBEMITTNSQIYQQHDWVLQYVDRTPITARHQIVLDLSQAAVR
DHLITTLINIVQNNQLDYLKWDMNRHLTQVGSTHLPAAQQGELYHRYVCGLYDILITRI
KRACFKLIIENCSAGGGRFDFGMLPYTNQTWISDLTDPVDRATIENGFSYLFPPRIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15324 ATGGCTAGTGCGCCGTTTACTTTCTTGCCAATCCTCTTAGGATTTTCAGCAACGAAGCGC 15265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NHITASPNAQNGRITPFETRLQLACIGQLGLELNPKQLAPSEQQLLRGALIKYQQLKS
TFIKAHFYRLPTTRHVVAWLIVTADKKQAICCYLNGLNSRVKTQHPLPLHYLDAELAY
SDSSGNRYTGHQLNTMGIPLKPTNADFTSQLIYLCQN"
                                                                                                                                  translation="MLLGAIEAGGTKFVCATGAENGQVSDRISIPTTTPVETMTAVDD"
                                                                                                                                                              YFTTHPVDAIGIGSFGPIGVNPHDPKYGYITTTPKPGWGDFDFLGHLKSQFNIPLYWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \bar{f} unction="enzyme II of the PTS system, sucrose specific"/note="enzyme IIabc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 TTCGGCGGCAATGAGTTCCTGGGCGCCGCTATTGGTATGGCGATGGTGTTCCCGAGCTT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 13; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 287.6; DB 1;
Pred. No. 4.3e-66;
; Mismatches 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVTNVQAGEQLVALTAPAASSVAATTV"
complement (15872. .15877)
                                                                                                                                                                                                                                                                                                                                                     complement (11673. .13832)
/gene="agas"
complement (11673. .13832)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (13852. .15989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (13852. .15807)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (15894. .15989)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                         GLLLAQAALKNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="scrA"
5993. .17568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="scrB"
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58.8%;
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QIFLIEBKHAEIVQIAIISKTKFPDNTTDQVARKVVTGLDLAFPARAGQVIPLAQOVNDP
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LYBLLERLITATA PHILFBGCSGGGREPAGMAYYMPOIWASDNTDAVARLTTOYGTSL
AYPISLATAHVSVSPNQOTGRETSKISTNSAVAASGVLGYELDITOLSSADKQIVQKQV
VQYKQIRPLAGFGSFRILKSPITSKOAAWWYSPOQDEAI VMYFNI.TSYAQFELTKTK
LVGINPKLNYQNI ATKALFGGDBLMQLGFYDPVVYQDYTKVYHFKAVTEN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IILLLLFTNLGGLYAKNAMIYLVVFAILYITMDIFYSFKDVGFWSMLPSLTTDSRERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTATFARLGSTIGGGLVGVLVMPAVIFFSAKATSTGDNRGWFIFALIICLIALISAWG
VGLGTREVDSDIRKNKQDTVGVMEIFKALAKNDQLLWAALAYLFYGVGINILGSLEVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TFAACTLGDGFAIKPSDGRILAPFDATVRQVFTTRHAVGLVGDNGIVLLIHIGLGTVK
LRGTGFISYVEEGQHVQQGDELLEFWDPTIKQAGLDDTVIMTVTNSTEFTMMDMLVKP
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                                                                                                                                                                                                                                                                                                         /function="raffinose transport protein"
note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8265. .8289
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/note="nR2", putative"

/rpt type=direct

10396...10442

/note="nR1; putative"

/rpt type=direct

10397...10443

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                                                                                                                                                                                                                                                                                                                                                                                 'codon_start=1
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   3909. .3914
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/note="putative"
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                                                                                                                                                                                                                                  1993. .5918
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OKLLTKLRLBDAKQRLSTSNNSVQSIANNVGYKDSFTFSKAFKRSGASPSYYRKSIG
Leenhouts, K.K.J., Bolhuis, A.A., Kok, J.J. and Venema, G.G. The sucrose and raffinose operons of Pediococcus pentosaceus PPE1.0 Unpublished
                                                                                            Direct Submission
Submitted (27-ARR-1994) Leenhouts K. K., Institute for Biological
Sciences, Department of Genetics, Kerklaan 30, Haren, The
Netherlands, 9751 NN
On May 26, 1994 this sequence version replaced gi:475962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="raffinose transport protein"
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standard name="regulator"
(citation=[1]
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/moi type="genomic DNA"
/strain="PPE1.0"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (2929, .3762)/gene="rafk"
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                                                                                                                                                                                                                                                                           /db_xref="taxon:1255"
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                                                                                                                                                                                                                                                                                                                                                                                                                  'rpt_type=INVERTED
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488...561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="DR1"
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                                                                                                                                                                                                                                                                                               87. .510
note="DR2"
                                                                                                                                                                                                                                                                                                                                                                                   note="IR1"
                                                                                                                                                                                                      .21839
                                                                               Leenhouts, K.K.
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           AUTHORS
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FEATURES
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insertion element; permease; regulator; sucrase.
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           TTCGGTGGCAACCCCTATCTGGGTGCTACG-ATGGGCATGATCATGGTCTTACCATCACT
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                                                                  GGTGAACGGCTACGACGTGGCCGCCACCATGGCTGCGGGCGAAATGCCAATGTGGTCCCT
                                                                                                  GTTTGGTTTAGATGTTGCCCAAGCCGGTTACCAGGGCACCGTGCTTCCTGTGCTGGTGGT
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Pediococcus pentosaceus
Bacteria: Firmicutes; Lactobacillaceae;
Pediococcus
1 (bases 1 to 21839)
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VAFAPDKIILNGGVNNQRQLFPMIRBKFAAYLNGYEEVPPLDDYIVPAGLGNNSGIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="scrA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303
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Pred. No. 4.3e-66;
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                                                                                                                                                                                                                                                                                                        'function="fructose 6-phosphotransferase"
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                                                                                                                                                                                                                                                                                                                                     standard name="fructokinase"
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/db.xref="G0A:P43470"
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                                                                                                                                     'standard name="terminator
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complement(10727. .11593)
                                                                                                                                                                                                                                              complement (10727. .11593)
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/gene="scrA"
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58.8%;
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                       'note="IR2"
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repeat_unit
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TGNKALDNRWYSLYLI INVLEX YELF IDFF CONAINERS ELECTIFIE FIREFUL
TGNKALDNRWYSLYLI INVLEX YELF IDFF CONAINERS ENCYGEWSMLP SLITTDSRERE
KTATFARLGGSTIGGGLYGWINNPAYI FFSAKATSTGDNRGWFIFALIT CLIALISAWG
VGLGTREVDSDIRKNYGDTVGWMEI FKALAKNDQLLWAALAYLFYGWGINILGSLEVY
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FYSSYQVOOGDHAVBLEPERSCSINYGTOT
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AYPISLATAHVSVSPNQOTGRETSMSTRSAVAASGVLGYELDLTQLSSADKQIVQKQV
VQYKQIRPLIQFGEFYRLKSPITSNQAAMMFVSPQQDBAIVMVFNLTSYAQPSLITKTK
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GLSNIQWGYRLNRSPSTISYELSRCQPYQAELAQTDABYKRSQCGRKYKLSDELKQKI
GLNILRLSWSPGMIAHEFKLATKSIYNWLNQCRIGESLNDLPEHGYRQRRNVDQRSKYN
QSLGRSIEQRPWHYDRNRIGDFLDTVVGFRGFRGFKJATLILIDRSSFRLMYSTRLKDR
TTATVNEALTKFLTTFNGFVHSFTVDRGTEFSGLNSLESQYGIKTYYCHAYTPADVVV
                                                                        translation="MQEEHNYKWVGGRLIYGFGAKGNDAFYSILSGYLIIFITSHLFD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="Swiss-Prot:P43467"
/translation="MSLITVDQANRVFHLHNQTLSYIPAVEQGGTLSHLYFGGHVDHY
HGELRYPRVDRGFSGNLPGSTDRTFSRDTLPKEYSTAGEMDYHLPAAIVRHTDGANAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVGLNPKLNYQNIATKAIFGGDELMQLGFYDPVVYQDYTTKVYHFKAVTEN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard name="IS-30 (E.coli) like IS element"
(standard name="IS-element"
(citation=[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _name="alpha-galactosidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="alpha-galactosidase"
fprotein_id="CAA83665.1"
db_xref="G1:475965"
db_xref="GOA:p43467"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8265. .8289
/standard_name="terminator 3"
/citation=[1]
                                              xref="Swiss-Prot:P43466"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="insertion element"
protein_id="CAA83666.1"
db_xref="GI:475966"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MNALIGIYVVFILKGLVLSTLVLKI"
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complement(9519. .10424)
/gene="iso-IS30"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (9519. .10424)
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'transl_table=11
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transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                               /gene="agax"
5976. 8177
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/gene="agaR"
/standard_nam
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/citation=[1]
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/note="DR2"
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/protein_id="MAK92528.1"
/db_xref="G1:15217138"
/fb_xref="G1:15217138"
/franslation="TypLipAltaGalthAlnNVLTGQGLFGAQSIVQMFPQWKGFAB
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IVNMMSSAPFTELPILIASATKREGGNYLGAAGAMLVMPNLVNGYGYABSIATGH
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MTLLADIAKTGGSPIVSNGYTDSLWARYQTGAGAMGFAPTFTRSFGLGYSAILTGAGISAMLGIT
FTLLADIAKTGGSPIPPUAMANIAQGAATFAVFTKWKQNGSLTTGSGLSAMLGIT
FDALFGYNIKLKFPFFGSTIGLASGISSFIIGLHVLSVSWGPAGIIGFIAIAPKSIPSF
MWGALISTVIAFVTYLYGKKAMKTTEBBIINBAPATSVURLQDBKISAPVTGRIV
DLASVPDPVPASEAMGKGIAIMPTSQDVLAPVTGYIVANTGGIGGABVLI
HIGHDTWNINGIGFFKLYGYGKAMKTTEBDLIGHFDIDKIKQAGITPLIMTIVINTAGYA

QVDPLITTUDKAAMQGBEIIQLHAKKD"
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VNAIWLSPVYQSPNVDNGYDISDYQAINPEYGSWVDWEQLIEAAKIRKIKIWDLVVV
HTSDQHPWFTEARKSKUNPYRDFYIRMDPATDGFYPNDLQSPRKGSAMAFDAVTGQYY
LHFYAKEQPDLNWQNPKVREAVYQMYTWWLQKGIGGFRMDVIDLIGKEPDRKIKENGP
QLHAYLQEMMARVLGSYDVVYTVGETWGATPEIGQMYSNPNRHELSMITOPFRIIKENGP
SGMTRWDLKPLIPAELHAVFSKWQLALDGVGWNSLFWSNHDLPRIVSRWGDDSQYREK
SAQALAIYLHMLKGTPYIYQGEBIGWTNYPITSYHBIBDIERRYYQQRQQGYAI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 TIGGIGAACGGCIACGACGIGGCCGCCACCAIGCGGCGGCGAAAIGCCAAIGIGGTCC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACTICCIGAICACICCAGIGCIGACGIIGCIGCICACCGGAIICCIIACAIICAICGCC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       382 GTTGCCTTCATTCTTGCTAATTTAGAGAAATTCTTCCATAAACATTTAAATGATGCTGTT 441
note="ScrA; similar to ScrA of Pediococcus pentosaceus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GICITIGGATICAAIATIGCGCAAGCIGGTIAICAAGGICAAGTAATICCGGITAICGGA
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Pred. No. 6e-57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="dextran glucosidase"
/protein_id="AAK92529.1"
/db_xref="G1:15217139"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="DexB; similar to DexB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                   /product="sucrose-specific
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trans1_table=
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/gene="dexB"
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|gene="dexB"
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/gene="dexB"
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ilarity 51.9%;
Conservative
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the PTS (scrA)
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Dudez,A.M., Chaillou,S., Hissler,L., Stentz,R.,
Chaillou,S., Alpert,C.A. and Zagorec,M.
Physical and genetic map of the Lactobacillus sakei 23K chromosome Microbiology 148 (Pt 2), 421-431 (2002)
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Dudez,A.-M., Chaillou,S. and Zagorec,M.
Direct Submission
Submitted (20-JUL-2001) Flore Lactique et Environnement Carne, INRA, Domaine de Wilvert, Jouy-en-Josas 78350, France
Location/Qualifiers
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/organism="Lactobacillus
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/db_xref="taxon:1599"
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Luesink, B.J., Marugg, J.D., Kuipers, O.P. and de Vos, W.M.
Characterization of the divergent sacRK and sacAR operons, involved
in sucrose utilization by Lactococcus lactis
J. Bacteriol. 181 (6), 1924-1926 (1999)
                                                   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (24-JUN-1997) Luesink E.J., Department of
Chemistry, Netherlands Institute for Dairy Research
Box 20, Ede 6714 BA, THE NETHERLANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .5800
/organism="Lactococcus lactis"
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/sub_species="cremoris"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      function="negative regulator"
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/db_xref="G1:4581475"
/db_xref="GOA:Q9S6S5"
/db_xref="TrBMBL:Q9S6S5"
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Luesink, E.J.
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KERDYLALLISNQVDGIIXGSHNLKAHDYIAIBAPIVAFDRILIFPETTVVSSDNFEGĞ
ILAFKALINGSGKKLAIFTANDNTNBSPYLRRDGYLLELBRQLKPHIIKIPSQWTLL
RKKVEIKKILENNDPGVFCTDDITAILVRDLASNLKKSLNVVGFDGTEFIENYYPNL
TTIKQPINDLAELLVDLIIRKIDGDNIDITYQLPYQLHYGID"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQLINLDEGFDCYATOSFNAPDGŜAYAISWLGIPETSYPTDKYNVOGYLSMYKKISIK
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YIPNAAARSLQGKSLKLIGLVFPTIKNIFYAELIEKIEQALFIRGYKAMLATTEHDEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LNDPNGFSYFNEKWHLFYQHPPFGPVHGLKSWVHLVSDDLVHFEKTGLVLYPDTKXDN
AGVYSGSALAFENFLFLIYTGNHRGEDWVRTPYQLGAKIDKNNQLVKFTEPLIYPDFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QTTDHFRDPQIFSFQGQIYCLIGAQSSQKNGIIKLYKAIENNLTDWKDLGNLDFSKEK
MGYMIECPNLIFINGRSVLVFCPQGLDKSIVKYDNIYPNYYIADDFTTGSKNQLKNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="sucrose-6-phosphate hydrolase"
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db_xref="GI:458196"
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Biophysical (NIZO), P.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (join (1283. .2704, 2721. .2725, 2737. .2743,
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complement(1416. .1422)
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complement(1416. .1422)
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sacK

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linear

Z97015.1 GI:4581474 enzyme II sucrose protein; fructokinase; sacA gene; sacB gene; sacR gene; sucrose-6-phosphate hydrolase.

Lactococcus lactis cremoris sucrose gene cluster. Z97015

5800 bp

LLZ97015

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ITNYQHSGIGGDFIFPVAACANMAQAGATFAILFVTKNIKTKALAAPAGVSAILGITE
BAFGAINLKKXPFFTALGASAIGSHPMLFHYLAVSHGSAGALIGFISTAGYTHQFM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IKYFKENRVGALGLGSFGPIDLALISSKTYGYITSTPKVGWKNINLVGQLKEALDIPIY
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TMSAAPFTFMPILLIGYSATKRFGGNPYLGAVVGMIMVMPGLINGYNVAEAISNHTWTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WDIFGFKVAQAGYQGQVLPVIGVAFILAKLERFFHKYLNDAIDFTFTPLLSVIITGFL
TFTIVGPALRFVSNGLTDGLVGLYNTLGALGMLVFGGFYSAIVVTGLHQSFPAIETML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEVLLHIGIDTVSMMCNGFIQNVKVGQKVKAGDLLGSFDKEEIKKSGLDDTVIIVITN
SASYNEILPLSENVDIKVGEKILLLIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'translation="MSVYYGSIEAGGTKFVLAIADEHFNIIKKFKFATTTPQETISKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="enzyme II sucrose protein"
protein id="CAB09690.1"
db_xref="GI:4581477"
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Pred. No. 3.3e-56;
0; Mismatches 647;
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protein_id="CAB09691.1"
db_xref="G1:4581478"
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/gene="sacB"
/evidence=experimental
2837. .2843
/gene="sacB"
/evidence=experimental
2872. .2877
/gene="sacR"
/evidence=experimental
complement(2721. .2725)
                                                                                                                                              complement (2761. .2767)
/gene="sacA"
                                                                                                                              'evidence=experimental
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                                                                                    complement (2737.
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/codon start=1
/transl_table=1:
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/gene="sack"
4838. .4842
/gene="sack"
4848. .5720
                                                                                                                                                                                                                2815. .4835 /
/gene="sacB"
2815. .2821
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51.1%;
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                                                                  gene="sacA"
                                                                                                        'gene="sacA"
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Matches 725; Conser
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TTTGGCGGAAATCCATATTTAGGTGCTG-TTGTAGGTATGATTATGGTGATGCCTGGACT
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                                                                                                                                                                                                                                                                                                                                                                                            244 ITCTTGGATTCTGGCAACGATCGAGAAGTTCCTGCACAAGCGACTCAAGGGCACTGCAGA
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/ translation="MOYPVTAKOLLESIGGKSNIQALAHCATRIRIVLMDETQINESA
IESLQGVKGQFKVAGQYQIIFGSGIVNQVYARMAKLTGLVEMSTNDVASAGAEKQNWA
QRAVKGLSDIFVRIIPAIVAGGLLMGLFNVLTAPGLFIEGQSLIDANFGLADLASMIN
                                                                                                                                                                                    TFTVVGPLTRDVGFMLGDALNWLYDSAGFVGGALFGFIYAPFVITGWHHSFIAIETQL
LADIVTTGGTFIPPLAAMSTAGGAAALAVGYWTKETKLKGYAIPSGYTALLGITFBA
MFGVNLKLRYPFIAALIGAALASAFITLFNVKAQALGAAGLPGIISINPQQIGYYIMG
MAISFVAAFALTVLLAMREKTKQAAQVTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="sucrose operon repressor SorR, putative"
/protein id="sakF96555.1"
/b_xref="d1:9658070"
/translation="WASLHDVRLAGVSKSTVSRVINDEYGVKESTKIKULKAVEQCG
YMVNQVAKDLKSQKTNLIGVIVPRVSSHATAQGVDGLTAIFEQAGKHVLLANTHQVHA
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LPEGYTEHIRDBRYYTYTGSKRQMLLGAADTLAHQBGRLAYYTBDDLLHHHEDKLYGDBLG
LDYGYWWECDDWFELGGEAFPVFGPQIASANPHHTIEHQNRIFRATONAQGEIALLCG
WPLDEGFDFYAPQTAQTADGRRVLCGWWGLPDFTQHPSCDQGWIHQITALREIEWREG
WPLDEGFDFYAPQTAGTADGRRVLCGWWGLPDFTQHPSCDQGWIHQITALREIEWRAG
TYQHPLREIDTLQSBFHTLLISDNYTELKTRSFALGYTLPWGCEIREMQNYCYRYTI
TYQHPLAENDLLDRAYNQIRQEDTIREILKLDSPTVEIRILADQSSLEIFINQGBHVWTS
RIFTPRDASGISLHGASVDAKLYYMAPASAPPNLEVNYQP"
                                                                                                                            TFANAPFVYLPVLLAFSASKKFGGNPFLGAALGMLMVHDDLLNGWGFGSASVSGTVPT
WNILGFEI EKVGXQGSVLPVLVSAYI LAKI ENGLRKI VPSVVDNLLTPMLAI FITGFL
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HYGFEAGGRUVKAGCKQIGFIGVQBDIAVDVLRSQGLQQALGPHQOTILFHARGNF
HINSGRQMAKQAYLDYPQLDGLFCATDRLAVGAIKLOGLGYHVGQQVKLLGVGNDEL
AYVSNPPLSTFNYAFDKAGENAAKMLLERIAGRGQEMSKVVLTPQNIQRETCPV"
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LOSVLGEWQLSVQRTAEVSDQQLAAIGKAIAERQKLETLPYQTALDCPYRPLMHISPP
QGLLNDPNGFIYHQGEYHLFYQWHPFACEHKDKYWVHLKSLDLVDWQWQSVALTPSDW
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GLQAIADFQIPLVVVTLGAKGALVVTPNSRQIVSGKAVKPIDTTGAGDAFVGGLLYRL
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VDLDEHGERSFTFMVKPSADQFLQLSDIPSFQNGEWLHVCSIALANQPSRSSTFAAIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                    note="similar to GB:L14685 PID:289864; identified
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/codon_start=1

/trans1_table=11
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/protein_id="AAF96556.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence similarity; putative"
/codon_start=1
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/db_xref="G1:9658072"
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/transl_table=11
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/gene="VCA0654"
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'qene="VCA0654"
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gene="VCA0655"
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/gene="VCA0655"
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/gene="VCA0657"
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/transl_table=
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4490 TAAATCTGGAGAACTTTTCTCACCAGCCGAGGAAATTATTATTGCTTATGAAACAGG 4549
                                                        1186 CCATGCTTTCGCAGTTCGCACCAAGGCTGAGGATGCTTCCAATGTGGATATCTTGATGCA 1245
                                                                                                                                                                        1246 CATTGGTTTCGACACAGTAAACCTCAACGGCACGCACTTTAACCCGGTGAAGCAGGG 1305
                                                                                                                                                                                                                                                                                              1306 CGATGAAGTCAAAGCAGGGGAGCTGCTGTGTAATTCGATATTGATGCCATTAAGGCTGC 1365
                                                                                                                                                                                                                                                                                                                                                            4658 CCAGAAAGTAAAAGCAGGGGATTTACTAGGATCTTTTGATAAAGAAGAAATCAAGAAGAG 4717
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                                                                                                                                                                                                                                               4657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCT 10-0CT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio cholerae Ol biovar eltor str. N16961 chromosome II, section AGO04395 AE003853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sucrose-specific IIBC component"
                                                                                                                                                                                                                                   4598 TATTIGGAATAGATACTGTTTCAATGAATGCTAATGGATTCATACAAAATGTTAAAGTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                     1366 AGGTTATGAGGTAACCACGCCGATTGTTGTTTCGAATT 1403
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Vibrio cholerae O1 biovar eltor str. N16961
                                                                                                                   4550 TCACGCTTATGGTATAAAAACAAAAATGGAGGT---
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/protein_id="AAF96554.1"
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/note="biotype: El Tor"
complement(114. .1553)
/gene="VCA0653"
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strain="N16961"
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/gene="VCA0653"
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PEWGYAPQKNTSVMPNAMTQPRSASYEDLRQYLLSNGIQHEVVPGDYPMIKLNNTVRF
ETGSAKVSMASKQWLDTVARFLATESGIDIVLEGHTDNTGSEKLNDKLAERRANAVKA
ALVQSRVAQNAIYTRGFGENVPACTNSTKNGRACNRRVEIRFILASN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MYTFALIKITLEQQAEMSAYTPSAQQEVLVGDHDQLVSTTDLKG
VITYCNDTFCRIAGFQADELLGKNHNIVRHASMPKAAFADMWHHLKQGHAWRGIVKNR
TKSGGFYWVDAYVTPIYQQGQLTGYQSVRVKAERKWVEIATKAYQALLAAEKAGKKIQ
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KYQNGRYDSIS ISRLIYGSGADAFSVADVHLKMASARIRTILGRAMDSARFDGELAMQLHI
TTQBYHQALAAQNSHTQAYDAYDAYDAYDASABRYGSHTRSAHQLIDOYQDHCAFTKHSI
NVTHQNLQRLATQAGSAALTTLKLSDQAQQVGQLMTBIGGIABCYNLLALNAAIBAAR
RGQGRGFARVYADBYRALLSARRQARAYQQIQTSIDTMLSTIRARRGDITASRDQTEQCA
QDANTTLQQLQDVBCYNSDMLRVIGBYASAAQHQRELTCEVNQHIHSIASVQTQNSAA
THTVEQLAMAMSGKVAEFGALSKQFAQK
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DAPLPGGENFDYAALKNQLVAAFPFITESVIERWLRSYGSRTTQLLAGVTGIEDLGIA
FSGELYQREIDYLCEKEFARHAQDIFWRRSKLGLNHDTSVVEEVESYLQQKFHAEQPL
                                                                                    /translation="mnarstretqdbuldlilugggingagiaadatgrglkvglyda
KDFASATSSASSKLVHGGLRYLEHYEFRLVSBALAEREVLLKKAPHIVTPMRFRLPHR
PFLRPAWMIRAGLFLYDNLGKRTSLPASHKVNLKAGSVTKPEWQIGFEYSDCWVDDAR
                                                                                                                                         LVIINAMQAQEQGAEVINYCTVEKAERMGDLWHVTLLDEQTQQRFERRSHALVNAAGP
WVKQFINENAHVSSPYGIRLIQGSHIIVPRIHDEPQAYILQNEDKRIVFVIPYLDDYS
MIGTTDVEYKGDPRKVAITDAERDYLISIVNKHFMREIARSDIIAEFSGVRPLCDDSS
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/protein_id="AAF96558.1"
/protein_id="AAF96558.1"
/tanslation:19658073"
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                                                                                                                                                                                                                                                                                                                                                                                                     product="methyl-accepting chemotaxis protein"
protein id="AAF96559.1"
db_xref="GI:9658074"
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'note="identified by Glimmer2; putative"
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protein id="AAF96560.1"
db xref="G1:9658075"
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0; Mismatches 387;
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/protein_id="AAF96561.1"
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The present invention relates to Corynebacteium glutamicum phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or related bacteria,

Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers

Claim 3; Page 98-101; 144pp; English.

typing or identify; for transformation

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126.6	126.6	126.6	126.6	121.4	121.4	114.6	113.4	111	109.6	109.6	109.4	108	107.8	107.8	107.8	105.6	103.6	103.6	66	86	97.8	97.2	93.6
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ALIGNMENTS

Haberhauer G; ds. Phosphoenolpyruvate; sugar phosphotransferase system; PTS; Zelder O, C.glutamicum phosphoenolpyruvate DNA #1. Schroeder H, BP. 99US-0142691P. 99US-0150310P. 99DE-01042095. 99DE-01042097. AAF31528 standard; DNA; 1527 27-JUN-2000; 2000WO-IB000973. Corynebacterium glutamicum. (first entry) Pompejus M, Kroeger B, WPI; 2001-080989/09 (BADI) BASF AG WO200102583-A2. 01-JUL-1999; 23-AUG-1999; 09-APR-2001 03-SEP-1999; 03-SEP-1999; 11-JAN-2001. AAF31528; RESULT 1 AAF31528

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                                                                                                         AGTITCTCCGGTGAGAGGAGGATTGTGTGGTGGCGATTCCCATCTGGCCATGCTTTCGCAGT
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The present invention relates to the isolation of Corynebacterium glutamicum metabolic pathway (MP) proteins, and the polynucleotide sequences encoding them. The MP proteins are enzymes involved in the metabolism of molecules important for the normal functioning of cells (e.g. amino acids, vitamins, cofactors, nucleotides and nucleosides, or trehalose). The polynucleotide sequences encoding the MP proteins are useful for producing fine chemicals, particularly organic acids, non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, (un) saturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes. The fine chemicals are useful in the food, animal feed, cosmetic or pharmaceutical industries. ABS65342-ABS65364 encode the C. glutamicum MP New metabolic pathway genes of Corynebacterium glutamicum for producing fine chemicals, e.g. lipids, (un)saturated fatty acids, vitamins, cofactors or enzymes used in food, feed, cosmetics or pharmaceutical Claim 1; Page 108-111; 176pp; English proteins of the invention P-PSDB; ABG80325 industries.

Sequence 1527 BP; 304 A; 392 C; 430 G; 401 T; 0 U; 0 Other;

0; 240 300 480 CGTITICGGCGCCAATGAGTTCCTGGGCGCCGCGTATTGGTATGGCGATGGTGTTCCCCGAG 120 120 180 240 300 360 360 420 480 540 540 600 099 CTTGGTGAACGGCTACGACGTGGCCGCCACCATGGCTGCGGGCGAAATGCCAATGTGGTC 180 420 600 099 9 9 CTCATGGCATCTGCGCCGTTCTTGCCAGTGTTGGTTTGGTTTCACCGCAACCAAG CCTGTTTGGTTTAGATGTTGCCCAAGCCGGTTACCAGGCACCGTGCTTCCTGTGCTGCTGCT AGACTICCTGATCACTCCAGTGCTGACGTTGCTGACCGGATTCCTTACATCATCGC GTTCTTCCTGGCGAAGAGTGAAAAGCTCAAGGGCCTTGCAGGGGCCTTGCAGGTGCTTCAGGTGTCTCCGC cerrrcegcescaardaerrceregecescerarregraregeargerereceaa CTTGGTGAACGGCTACGACGTGGCCACCATGGCTGCGGGAAATGCCAATGTGGTC CCTGTTTGGTTTAGATGTTGCCCAAGCCGGTTACCAGGGCACCGTGCTTCCTGTGCTGGT GGTTTCTTGGATTCTGGCAACGATCGAGAAGTTCCTGCACAAGCGACTCAAGGGCACTGC AGACTTCCTGATCACTCCAGTGCTGACGTTGCTCACCGGATTCCTTACATCGC CATTGGCCCAGCAATGCGCTGGGTGGCGATGTGCCTGGCACACGGTCTACAGGGACTTTA TGATTTCGGTGGTCCAGTCGGCGGTCTGCTTCGGTCTGGTCTACTCACCAATCGTCAT CACTGGTCTGCACCAGTCCTTCCCGCCAATTGAGCTGGAGCTGTTTAACCAGGGTGGATC CTTCATCTTCGCAACGGCATCTATGGCTAATATCGCCCAGGGTGCGGCATGTTTGGCAGT GITCITCCTGGCGAAGAGTGAAAAGCICAAGGGCCITGCAGGTGCITCAGGTGTCTCCGC Gaps CACTGGTCTGCACCAGTCCTTCCCGCCAATTGAGCTGGAGCTGTTTAACCAGGGTGGATC CTTCATCTTCGCAACGCCATCTATGGCTAATATCGCCCAGGGTGCGGCATGTTTGGCAGT 0,5 DB 6; Length 1527; Indels 0 100.0%; Score 1527; 100.0%; Pred. No. 0; live 0; Mismatches Query Match
Best Local Similarity 100.
Matches 1527; Conservative 121 61 61 121 181 181 241 241 301 301 361 361 421 421 481 541 541 601 601 481 ò g 음 g Db g g $\stackrel{>}{\circ}$ g $\overset{\diamond}{\circ}$ ઠે ð δ g ò g ò d ð δ 8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
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Ozaki A;
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Ikeda M,
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                          glutamicum.
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Best Local Similarity 99.9
Matches 1526; Conservative
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Senoh A,
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Pred. No. 0;
0; Mismatches 0; Indels 1.
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la M, Ozaki A;
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07-APR-2000; 2000JP-00159162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene encoding sucrose phosphoenolpyruvate-sugar transport system enzyme II obtained by cassette ligation-mediated amplification of downstream domain of coryneform bacterium sucrase gene, with sucrose-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence encodes the Brevibacterium lactofermentum sucrose
 AGTAAACCTCAACGGCACGCACTTTAACCCGCTGAAGAAGCAGGGCGATGAAGTCAAAGC
              AGGGGAGCTGCTGTGTGATTTCGATATTGATGCCATTAAGGCTGCAGGTTATGAGGTAAC
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                                                                                                                              Brevibacterium lactofermentum; sucrose PTS enzyme II; sucrase; phosphoenolpyruvate:carbohydrate phosphotransferase system; glucose; coryneform bacterium; phosphoenolpyruvate-sugar transport system; ds.
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                                                                                                                                                                        The present invention relates to Corynebacteium glutamicum phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for
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Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation.
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Pred. No. 0;
0; Mismatches
                                                                                                                             Page 103-104; 144pp; English
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2151 ACAGGTGGTTCATTTATCTTCCCAATGCAACGATGTCAAATATTGCACAAGGTGGTGCTGCA 2092
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                                                                                                                                                                                                                    242 GITICITGGAITCIGGCAACGAICGAGAAGTICCTGCACAAGCGACTCAAGGGCACTGCA 301
                                                                                                                                                                                                                                                                                                                                  302 GACTICCIGAICACTCCAGIGCIGACGIIGCIGCICACCGGAIICCIIACALICALCGC 361
                                                                                                                                                      2511 Grefriggeciacatartaargaagragstaricaggacaagrarraccrargera
                                                                                                     CTGTTTGGTTTAGATGTTGCCCAAGCCGGTTACCAGGGCACCGTGCTTCCTGTGCTGGTG
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To vaccination. The nucleic acids (I) may be used to produce the S.

The polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the creatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polypurcleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in the secuence listing of the present invention. N.B. The present invention sequence listing of the present specification, however the sequence of listing only goes up to SEQ ID NO:4454 so even though sequences are given the contains and in the form the present should be accenting the present specification of the present specification, however the sequence of the present specification, however the sequence of the present specification, however the sequence of the present specification, however the sequence of the present specification, however the sequence of the present specification, however the sequence of the present specification of the present specification of the present specification of the present specification of the present specification of the present specification of the present specification of the sequence are given in the sequence of the present specification of the present specification of the sequence are given in the sequence of the present specification of the sequence are given in t
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                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
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                                                                                                                                                                                                                                                                                                                         S. epidermidis genomic polynucleotide sequence SEQ ID NO:3464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2913 BP; 1072 A; 480 C; 419 G; 942 T; 0 U; 0 Other;
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82988 GTTACTAAGAGATAATTATTGATAAGTAAAATCAAAA 83023
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Pred. No. 1.7e-45;
0; Mismatches 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 1030-1031; 2188pp; English
                                                                                                                 AAH54100/c
ID AAH54100 standard; DNA; 2913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus epidermidis.
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                                                                                                                                                                                                                                                               03-SEP-2001
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                                                                                                                                                                                                       AAH54100;
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The invention describes a method of monitoring differential expression of genes in a first Bacillus cells relative to expression of the genes in other Bacillus cells, comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus genomic sequenced tags (GST), examining the array, and determining relative gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cells relative to expression of the same genes in one or more second Bacillus cells. The method is useful for monitoring global expression of several genes from a Bacillus cell, discovering new genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way in which Bacillus cells adapt to changes in culture conditions, environmental stress or other physiclogical provocation. Extensive follow cup characterisation is unnecessary, when one spot on an array equals one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 GITICGGCGGCAAIGAGIICCIGGGCGCCGCGIAIIGGIAIGGCGAIGGIGITCCCCGAGC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene or one open reading frame, since sequence information is available. This sequence represents a genomic sequence tag (GST) used in the method of the invention. Note: The sequence data for this patent did not form
                                                                                                                                                                                                                                       Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               but was obtained in electronic format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   part of the printed specification, but was obtained in electror directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 975;
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                                                                                                                                                                                                                                                                                                                                                            Claim 4; SEQ ID NO 829; 200pp; English
                                                                                    BIOTECH INC.
                  2000US-00680598.
2001US-0279526P.
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Best Local Similarity 52.6
Matches 437; Conservative
                                                                                                                                                       Clausen IG;
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                                                                                    NOVOZYMES NOVOZYMES
                  06-OCT-2000;
27-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein, useful as a vaccine for treating or infection, specifically an infection caused by
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GATITCGGTGGTCCAGTCGGCGGTCTTCGGTCTGGTCTACTCACCAATCGTCATC
                              GAACAATTCGCCGTACTGGGCGGACTGTTATACGGAGGGCTTTACGCCGCTCTCGTCATT
                                                           ACTGGTCTGCACCAGTCCTTCCCGCCAATTGAGCTGGAGCTGTTT-----AACCAGGGT
                                                                                                                           GGATCCTTCATCTTCGCAACGGCATCTATGGCTAATATCGCCCAGGGTGCGGCATGTTTG
                                                                                                                                                                                      GCAGTGTTCTTCCTGGCGAAGAGTGAAAGCTCAAGGGCCTTGCAGGTGCTTCAGGTGTC
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                                                                                             526 ACCGGAATGCATCATACATTCCTTGCCGTTGACCTTCAGCTGATCGGCTCAAAGCTCGGC
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P-PSDB; ABM72990.
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Bush D;
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                                           Enterococcus faecalis.
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                                                                                                                                                                                                      Dougette-Stamm LA,
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                                                                                                                                                                 (DOUC/) DOUCETT
(BUSH/) BUSH D.
                                                                                                                13-AUG-1998;
                                                                                                                                          15-AUG-1997;
                                                                  JS6617156-B1
                                                                                          09-SEP-2003
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used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus genes of the invention
                                                                                                                                                                                                                        CTCAAGGGCACTGCAGACTTCCTGATCACTCCAGTGCTGACGTTGCTGCTCACCGGATTC
                                                                                                                                                                       227 CITCCIGIGCIGGIGGTITCTIGGATTCTGGCAACGATCGAGAGTTCCTGCACAAGCGA
                                                                                                                                                                                                                                                                                                                     CTACAGGGACTTTATGATTTCGGTGGTCCAGTCGGCGGTCTGCTCTTCGGTCTGGTCTAC
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                                                                                                    15;
                                                Sequence 861 BP; 259 A; 136 C; 171 G; 295 T; 0 U; 0 Other;
                                                                                                  Indels
                                                                        11.4%; Score 174.6; DB 8; 54.2%; Pred. No. 5.2e-41; ive 0; Mismatches 329;
                                                                                                                                                                                                                                                                                                                                                                     467 TCACCAATCGTCATCACTGGTCTGCACCAGTCCTT
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The invention relates to Enterococcus faecalis polynucleotides and polypeptides. The invention also relates to a recombinant expression vector comprising a polynucleotide operably linked to a transcription regulatory element, a cell comprising a recombinant vector, a method for producing an E. faecalis polymeptide, an isolated nucleic acid comprising a sequence not given in the specification, a recombinant vector comprising the nucleic acid and a cell comprising the recombinant vector. The polynucleotides can be used to detect the presence of E. faecalis in a sample. The sequences are useful for preparing a composition for diagnosing or treating Enterococcus faecalis infection. This sequence
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Enterococcus faecalis infection; transcription regulatory element; antibacterial; gene; ds.
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Pred. No. 5.5e-40;
0; Mismatches 624;
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97US-0044031P. 97US-0046655P. 97US-0066009P.

98WO-US008985

us-09-604-231-1.rng

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(HUMA-) HUMAN
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16-MAY-1997;
14-NOV-1997;
                                                                                                   04-MAY-1998;
                                   12-NOV-1998
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Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
                                                                                                                                                                         faecalis genome contig SEQ ID NO:31
                                            5840
                                                                                                                               (first entry)
                                         AAX12968 standard; DNA;
                                                                                                                                                                                                                                                                                    Enterococcus faecalis
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3,
                                                                                                                                                                                                                                                                             A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAX12938 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcus faecalis in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by creamism can be used in vaccines to prevent or attenuate an Enterococcal infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                            New isolated Enterococcus faecalis polynucleotides and polypeptides used to develop products for the detection of Enterococcus and for vaccines for prevention or attenuation of Enterococcus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5840 BP; 1848 A; 944 C; 1256 G; 1779 T; 0 U; 13 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
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Pred. No. 1.4e-33;
0; Mismatches 533;
                                                                                                                                                                                                                                     Claim 1; Page 389-392; 2084pp; English
Barash SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.9%;
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      Dillon PJ,
                                                       WPI; 1999-045171/04
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Best Local Similarity
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KUNSCH C A. DILLON P J.

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                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a new computer readable medium with an Enterococcus faecalis nucleotide sequence. The invention is useful to diagnose the presence of E.faecalis in a sample or determining the presence of a specific microbe in a sample. The invention is also useful for modulating the growth or pathogenicity of E.faecalis, in a vaccine to confer resistance to Enterococcal infection, for commercial, therapeutic and industrial purposes, and for fermenting a particular sugar source or to produce a particular metabolite. The invention is useful for detecting diseases related to Enterococcus infections in animals, and for detecting E.faecalis using biochip technology. The present nucleic acid sequence represents an Enterococcus faecalis contig DNA sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO
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                                                                                                                                          Computer readable medium having recorded on it a Enterococcus faecalis nucleotide sequence useful for detecting diseases related to Enterococcus infections in animals.
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                   for
 GGCAGCATTGATCCAGATGCAACCGCTGCTGCTGCAGGAACGACCAAAGCCGAA 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful paring a vaccine composition against Klebsiella pneumoniae.
                                                          ATGGTGGCACCTGTAAAAACGAATCAAGAAGACAAAATTATTTTAGCAAGTCCACTTCAA
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                           vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This sequence encodes a Klebsiella pneumoniae. The sequence encodes a Klebsiella
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llarity 51.3%; Pred. No. 1.2e-31;
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1; 1057 1117 1177 The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element, and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This sequence encodes a Klebsiella pneumoniae polypeptide of the invention 1178 TTTCGGCGATGCTGGGGATCACCGAGGCGAATCTTCGGGGATTAACCTGCGCTTTGTGA 1237 242 useful for 757 302 817 362 877 TTGGCCCAGCAATGCGCTGGGTGGGCGATGTGCTGGCACACGGTCTACAGGGACTTTATG 422 482 997 533 593 653 TGGCAGTGTTCTTCCTGGCGAAGAGGTGAAAAGCTCAAGGCCTTGCAGGTGCTTCAGGTG rcircecarcaacidecearcarcecraccacecaccercraccecracrecrac 243 ITTCTTGGATTCTGGCAACGATCGAGAAGTTCCTGCACAAGCGACTCAAGGGCACTGCAG CGGTGTGTTTATGAGGATCGAGAAAGCGGCTGCCGCGTGATCCCTGACGCGCTGG rcieccicedecearcidedecicades de la respectation de la reconstruction de l TTGCGGTGTGTTAAAACCAAAGATGCCAAAATAAAAGCTATCACCCTGCCGTCGCGT TGTTTGGTTTAGATGTTGCCCAAGCCGGTTACCAGGGCACCGTGCTTCCTGTGCTGGTGG ACTICCIGATCACTCCAGTGCTGACGTTGCTGCTCACCGGATTCCTTACATCGCCA Accigarcerectedenereliaiiiiiiiiiiaice ATTICGGIGGICCAGICGGCGGICTGTTCGGICTGGTCTACICACCAATCGICATCA 938 GCCACGCCGGCTGGCTGGCGGCCTGCTTCGGCGGCCTCTATTCGGTGATCGTTATTA 99-----998 ccáciniccarcaccirccaraccarcaacaacacacacacaaccarcarra GIGGAICCTICAICTICGCAACGGCAICTAIGGCTAATAICGCCCAGGGIGCGCAIGIT 1058 GCGTCAACTTCCTGCTGCCGATCTGGGCGATGGCCAACGTCGCCCAGGGCGGCGCCTGCT TCTCCGCTGTTCTTGGTATTACGGAGCCTGCGATCTTCGGTGTGAACCTTCGCCTGCGCT Gaps ds. 9. acid encoding a Klebsiella pneumoniae polypeptide, vaccine composition against Klebsiella pneumoniae. DB 11; Length 1452; Klebsiella pneumoniae protein; antibacterial; Vaccine; gene; Sequence 1452 BP; 256 A; 452 C; 429 G; 315 T; 0 U; 0 Other; CTGGTCTGCACCAGTCCTTCCCGCCAATTGAGCTGGAGCTGTTTAACCA-9.4%; Score 143.6; DB 11; Length 51.3%; Pred. No. 1.2e-31; cive 0; Mismatches 339; Indels Disclosure; SEQ ID NO 5847; 932pp; English (GENO-) GENOME THERAPEUTICS CORP 99US-0117747P 27-JAN-2000; 2000US-00489039 Best Local Similarity 51.3 Matches 366; Conservative Osborne M; Klebsiella pneumoniae WPI; 2003-895346/82 Local Similarity P-PSDB; ABO66501 29-JAN-1999; US6610836-B1 New nucleic preparing a 26-AUG-2003 Breton GL, 869 818 878 534 1118 183 303 594 654 363 423 Query Match 483 ö ద qq 엄 g ⋧ à g à 엄 ò δ ð δ g

Search completed: October 30, 2004, 14:04:57 Job time: 734 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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October 30, 2004, 13:46:16; Search time 154 Seconds (without alignments) 7047.887 Million cell updates/sec nucleic search, using sw model OM nucleic Run on:

US-09-604-231-1 1527 Title: Perfect score:

1 ctcatggcatctgcgccgtt......gttgaaaccttgagtgttcg 1527 Sequence:

Scoring table:

824507 seqs, 355394441 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched:

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 3464. Ap	2417.		5847		297. 7	201	463.	Sequence 2077, Ap	17.	-	17,			Sequence 2847. Ap			0	1806,	56, A		1876.		1317.	13	9	24
SUMMARIES	ID	US-09-710-279-3464	US-09-134-000C-2417	US-09-489-039A-6203	US-09-489-039A-5847	US-09-134-001C-1277	US-09-583-110-297	US-08-961-527-201	US-09-583-110-463	US-09-134-000C-2077	US-08-920-812-17	US-08-920-827-17	US-08-921-177-17	US-08-362-577C-17	US-08-920-828-17	US-09-543-681A-2847	US-08-961-527-30	US-08-673-190A-3	US-09-489-039A-1041	US-09-489-039A-1806	US-08-956-171E-56	US-08-781-986A-56	US-09-107-532A-1876	US-09-107-532A-1634	US-08-956-171E-1317	-80-	-08	US-09-134-000C-2419
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                                    Sequence 3464, Application US/09710279
Bettent No. 6703492
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERENCE: PU3480US
CURRENT APPLICATION NUMBER: 0S/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR PLING DATE: 1999-111-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN VET. 2.1
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Pred. No. 3.7e-48;
0; Mismatches 364; Indels
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Best Local Similarity 55.0%; Pre
Matches 468; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
RESULT 1
US-09-710-279-3464/c
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LENGTH: 2913
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREDVOLARE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION UNDER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
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9.4%; Score 143.6; DB 4;
Best Local Similarity 51.3%; Pred. No. 7.9e-34;
Matches 366; Conservative 0; Mismatches 339;
                                             Sequence 5847, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
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          US-09-489-039A-5847
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US-09-489-039A-5847
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                            Sequence 6203, Application US/09489039A
Patent No. 6510836
EAGHORN 6510836
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US 60/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 6203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.4%; Score 143.6; DB 4;
Best Local Similarity 51.3%; Pred. No. 7.7e-34;
Matches 366; Conservative 0; Mismatches 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6203/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-489-039A-6203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1386
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302 817

Gaps

877 422 937 482

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APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Poeumoniae for Diagnostics and Therapeutics
FILE REPERBERGE: PATHOU-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR PILING DATE: 1998-05-12
PRIOR PILING DATE: 1998-05-12
PRIOR PILING DATE: 1998-05-12
PRIOR PILING DATE: 1998-05-12
NUMBER OF SEQ ID NOS: 5322
SEQ ID NOS: 5322
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Pred. No. 1.7e-28;
0; Mismatches 629;
           ; Sequence 297, Application US/09583110
; Patent No. 6699703
                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA; ORGANISM: Streptococcus pneumoniae US-09-583-110-297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.3%;
Best Local Similarity 47.0%;
Matches 581; Conservative
                                                               GENERAL INFORMATION:
-09-583-110-297
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                                                    Sequence 1277, Application US/09134001C

Patent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-01-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1277
LENGTH: 732
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; OTHER INFORMATION: Identity of nucleotide at the above locations are US-09-134-001C-1277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 732;
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Pred. No. 4.2e-32;
0; Mismatches 221;
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cal Similarity 56.4%;
305; Conservative
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TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 201:
SEQUENCE CHARACTERISTICS:
LENGTH: 3895 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                     8.3%;
                                                                                                                                                                  Conservative
                                                                                          linear
                                                                                                                                                  Similarity
                                                                                       ; TOPOLOGY:
US-08-961-527-201
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Matches 575;
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Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
1435
                                                                                                                              ATACGAACTTGCAGCAGAATTCGTTGCTCAAGAAGCAGAATTTGTGAGCCATGAAC 1495
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                                          TCGGCGCAGCGATTGCTTATGGCCTTTACTTGGTTCGCCGCAACGGCAGCATTGATCCAG
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Genome Sciences, Inc
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSDOS version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
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CURRENT APPLICATION DATA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: HP Vect OPERATING SYSTEM:
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                                                                                                                                                  190 TITAGATGTTGCCCAAGCCGGTTACCAGGCACCGTGCTTCCTGTGCTGGTGGTTTCTTG
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                                                                                   Gaps
                                                                               27;
Score 126.6; DB 4; Length 3895;
Pred. No. 2.6e-28;
0; Mismatches 619; Indels 27;
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509 ATTGAGGTGGAGCTGTTTAACCAGGGTGGATCCTTCATCTTGGCAACGCCATCTATG 565	566 GCTBATATCGCCCAGGGGGGGGTGTTTGGCAGTGTTCTTCCTGGGGAAGAGGGAAGAGGGGSGAAGAGGGSGGGGGGGGGG	626 CTCAAGGGCCTTGCAGGTGTTTCAGGTGTCTCCGCTGTTTTTGGTATTACGGAGCCTGCG 685	686 AICHTOGGIGIGAACCTICGCCIGGCCGTTCTTCAICGGTAICGGTACCGCAGCT 745	746 AICGGIGGCGCITIGAITGCACTCTITAATAICAAGGCAGTTGCGITGGGCGCTGCAGGT 805	806 ITCTIGGGIGTICTATIGAIGCICCAGAIAIGGTCAIGTTCTIGGIGIGGGGTT 865 1240 AICCCIGGIACAAIGGTITAIGTIGGIAACGGACAACACAATACCTICTAIGGIA 1299	866 GITACCITCITCAICGCAITCGCGCACGAITGCTITAGGCCTITACITGGITCGCCGC 925	926 AACGGCAGCATTGATCCAGATGCACCGCTGCTCCAGTGCCTGCAGGAACGACCAAAGCC 985	986 GAAGCAGAAAGCACCCGGCAGAATTTTCAAACGATTCCACCATCCAT	1046 GGTGAAGCTATTGCACTGAGCGTCAGCGATGCCATGTTTGCCAGGGAAAGCTTGGC 1105	1106 TCGGGCGTTGCCATCGTCCCAACGGGCAGTTAGTTTCTCCGGTGAGGATT 1165	1166 GIGGIGGCAITCCCAICTIGGCAIGCITTCGCAGTICGCCCAAGGCTGAGGAIGGITCC 1225 1579 ICAAITGCCITTCCAACAGGGCACGCTITTGGTITGAAAACAAGAAATG 1627	1226 AAIGTGGATATCTTGATGCACATTGGTTTCGACACGCTAAAGCCTCAACGGCACGCAC	AACCCGCTGAAGAAGCAGGGCGATGAAGTCAAAGCAGGGGAGCTGCTGTGAATTCGAT 	1346 ATTGATGCCATTAAGGCTGCAGGTTATGAGGTAACCAGGCCGATTGTTTTTTTT	1406 AAGAAAACGGACCTGTAAACACTTACGGTTTGGGCGAAATTGAAGCGGGGGCAACCTG 1465 1807 GCTGACTACAGTAGCTCCAGTCGCAACAGGTTCAGTTGCGAAGGGGATGCTGT 1866	1466 CTCAACGTCGCAAAGAAA 1483 	RESULT 9 US-09-134-000C-2077 ; Sequence 2077, Application US/09134000C ; Patent No. 6617156
λ δ	S P	Qy	VQ QD	\$ G	Sy do	S G	දු දු	& A	Š da	Qy Db	QY	QV Dp	QY QD	VV PP	Qy Up	QV QD	RES US-
QY 1081 CATGITIGCCAGCGGAAAGCTIGGCTCGGCGTTGCCATCCCAACCAACGAGGGCGGTT 1140 Db 2324 TAITITIGCATCAGGGGTGTCAGGGGCAAGGTCTAGTCATCAAGCCAAGGTGAGTT 2265	OY 1141 AGTITCTCCGGTGAGTGGAAAGATTGTGGTGGCATTCCCATCTGGCCATGCTTTCGCAGT 1200 Db 2264 GACCTCTCCAGTTAATGGGACAGTGACGGTTCTTTTCCCTACCAAGCATGGGCAT 2205	OX 1201 TGGCACCAAGGTGGATGGTTCCAATGTGGATATCTTGATGCACTTTCGACAC 1260 Db 2204 TGTCTCTGACGAGGAGTTGAATTGCTCATCCACATCGGTATGGATAC 2157	OY 1261 AGTAAACCTCAACGGCACGTCCTTAACCGCTGAAGAAGAGGGGGGTGAAGTCAAAGC 1320 Db 2156 AGTAGGTCTTGATGGCAAAGGTTTTGAAAGTCTTGTAGTCCAAGGAGAGATCACGTTACAGT 2097	2y 1321 AGGGAGCTGCTGTGAATTCGATATTGATGCCATTAAGGCTGCAGGTTATGAGGTAAC 1380 Db 2096 TGGTCAGCAACTGATTCGTTTTGATATGATGTCATTAAGGCTGCAGGTCTGCTGCAGA 2037	OY 1381 CACGCCGATTGTTTCGAA 1401 Db 2036 AACTCCTGTTATCACCAA 2016	RESULT 8 US-09-583-110-463	; Sequence 463, Application US/09583110 ; Patent No. 6699703 ; RENERAL INFORMATION: ; APPLICANT: LVnn Doucette-Stamm et al.	NVENTION: N NVENTION: F ENCE: PATHC PLICATION NU	92 E	; PRIOR FILING DATE: 1998-05-12 ; PRIOR PRILING NUMBER: US 60/051,553 ; PRIOR FILING DATE: 1997-02 ; NUMBER OF SEQ ID NOS: 5322	; SEQ ID NO 463 ; LENGTH: 1884 ; TYPE: DNA ; ORGANISM: Streptococcus pneumoniae	Os-09-583-110-483 Query Match 7.7%; Score 117.6; DB 4; Length 1884; Best Local Similarity 46.4%; Pred. No. 1e-25; Match Constanting 10. Minmatch 20. 1748 5.	Vally Corrections 597 index 597 car. Car. Car. Car. Car. Car. Car. Car. C	269 AAGTICCIGCACAAAGCGACTCAAGGCCACTGCAGACTICCTGATCACTCCAGTGCTGACG	Db 700 AAAGCTGTCCGCAAGGTTGTTCCAGATGTCATTGACCTCTTGGTAACACCATTCGTGACA 759 Qy 329 TTGCTGCTCACGGATTCCTTACATTCATCGCCATTGGCCCAGCAATGCGCTGGGTGGG	389 GAIGTGGCACACGGTCTACAGGGACTTTATGATTTCGGTGGTCCAGTCGGCGGTTGGCGGGGTTTGGTTGG	Qy 449 CICTICGGICIACICACCAAICGICATCACTGGICIGCACCAGGCCAGCCA 508 B80 IIGAIIGGIGGGGITCACCAAIIGAICGIGTCAGGIGTGCACCACATCTICAACTIG 939

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Sequence 17, Application US/08920812
Patent No. 5763188
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; STRAIN: Clinical Isolate EC-24
US-08-920-812-17
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REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 3615 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TELEFAX: 312/474-0448
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                            RESULT 10
US-08-920-812-17/c
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Best Local (
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BATEROCCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR PILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTH VEFRION 3.1
LENGTH: 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1004 GAATTITCAAACGATICCACCAICAICCAGGCA---CCTTIGACCGGIGAAGCTATIGCA 1060
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                                                                                                                                                                                                                                                                                                                                                                                                                        24; Gaps
                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.5%; Score 114.6; DB 4; Length 951; Best Local Similarity 48.4%; Pred. No. 5.5e-25; Matches 429; Conservative 0; Mismatches 434; Indels 24
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                                                                                                                                                                                                                                                                                               ORGANISM: Enterococcus faecalis
US-09-134-000C-2077
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1301 CAGGGCGATGAAGTCAAAGCAGGGGAGCTGCTGTGAATTCGATATTGATGCCATTAAG 1360
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                                                        769 CAAGGIGATICIGITAAAAAGGAGATITGCTAGTIACTITICATATIGCTGCCATIAAA 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312 TCACTCCAGTGCTGACGTTGCTGCTCACCGGATTCCTTACATTCATCGCCCATTGGCCCAG 371
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                                                                                                                        1361 GCTGCAGGTTATGAGGTAACCACGCCGATTGTTGTTTCGAATTACAA 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
APPLICANT: Eda, Soji
APLICANT: Pache for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
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                                                                                                                                                                                    829 daadcirdriarccdgraginacaccdarrcraginacdaa
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ParentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,812
WTI.ING DATE: 29-AUG-1997
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COUNTRY: United States of America
ZIP: 60606-6402
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APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
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Sequence 17, Application US/08920827
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RESULT 11 US-08-920-827-17/c

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                                                                 APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                    Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gerstein, Murray &
South Wacker Drive
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Pred. No. 4.4e-23;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,827
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
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APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-WAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
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STRAIN: Clinical Isolate EC-24
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ADDRESSEE: Marshall, O'Toole,
STREET: 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
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TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 25-3856
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 3615 base pairs
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Best Local Similarity 46.3
Matches 540; Conservative
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STRANDEDNESS: double
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Patent No. 5770375
GENERAL INFORMATION:
APPLICANT: Obno, 7
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                   6300 Sears Tower, 233 South Wacker Drive
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46.3%; Pred. No. 4.4e-23;
tive 0; Mismatches 589;
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/921,177
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION DATE:
BYOR APPLICATION DATE:
FILING DATE: 27-MAR-1995
ATTORNEY, AGENT INFORMATION:
NAME: Rin-Laures, 11-Hsien
REGISTRATION NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 312/474-6300
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                                          CITY: Chicase STATE: Illinois COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/921,177
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STRAIN: Clinical Isolate EC-24
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Matches 540; Conservative
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MEDIUM TYPE: Floppy
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APPLICANT: Ohno, Tsuneya
APPLICANT: Matanisa, Akio
APPLICANT: Wehara, Hirotsugu
APPLICANT: Bda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
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APPLICANT: Ohno, Tsuneya APPLICANT: Watsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
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APPLICANT: Otho, Tsuneya
APPLICANT: Otho, Tsuneya
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDEMENTE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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; Sequence 17, Application US/08362577C
; Patent No. 5807673
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                                                                                                                                                                                                                     NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REPERENCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 11874-6300
TELEFRAK: 312/474-0448
US/08/362,577C
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STRAIN: Clinical Isolate EC-24
US-08-362-577C-17
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                                                     27-MAR-1995
                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3615 base pairs
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     APPLICATION NUMBER:
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STRANDEDNESS: doub
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TOPOLOGY: 11 MOLECULE TYPE:
                                                                                            TYPE: nuclei
STRANDEDNESS:
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REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
TELEPHONE: 312/474-6300
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COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-WAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17, Application US/08920828
Patent No. 585398
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Wetsuhisa, Akio
APPLICANT: Batsuhisa, Akio
TITLE OF INVENTION: Probe for Diagn
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Ger
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,828
FILING DATE: 29-AUG-1997
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312/474-0448
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STREET: 600
TTW: Chicago
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Pred. No. 4.4
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STRAIN: Clinical Isolate EC-24
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Best Local Similarity 46.3%;
Matches 540; Conservative
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                                                                          MULNUL 1815 base pairs
LENGTH: 3615 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
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Sequence 2847, Application US/09543681A

Patent No. 6605709

GENERAL INPORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
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CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 2847
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; ORGANISM: Proteus mirabilis
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US-09-543-681A-2847
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Sequence 1, Appli
Sequence 2904, Ap
Sequence 829, App
Sequence 31, Appl
Sequence 359, App
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10523.989 Million cell updates/sec
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                                                                                                                                                                    October 30, 2004, 15:50:57; Search time 744 Seconds
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| cgm2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgm2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgm2_6/ptodata/1/pubpna/US06_DNEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Sequence 9369. An	Segmence 152. App	Sequence 30. Appl	30	822	734	857	71	27	Sequence 24691. A	Seguence 34025. A	Sequence 56, Appl	Sequence 56, Appl	Sequence 1040, Ap				893	131	13	0	Sequence 21444. A	Sequence 38846, A	36728,		Sequence 799, App		Sequence 39556. A	Sequence 5313. An	ďΩ	(1)		Sequence 163, App
US-09-815-242-9369	US-10-	US-08-961-527-30	US-1	US-09-974-300-822	10S-05	US-09-974-300-85		us	US-10-282-122A-24	US-10-282-122A-3402	US-08-781-986A-56	Þ					US-09-974-300-893	US-08-781-986A-	US-10-329-624-13	₽		US-10-282-122A-3884		US-09-070-927A-550	US-09-974	US-09	US-10-28	US-09-974-300-5313	US-10-282-122A-1		US-08-961-527-163	US-10-158-844-163
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7.4	7.1	7.1	7.1	6.9	6.5	6.4	6.1	6.1	6.1	5.7	5.6	5.6	5.3	5.3	5.2	5.1	5.0	5.0	5.0	4.0	4.8	4.7	4.7	4.6	4.6	4.5	4.5	4.5	4.4	4.4	4.4	4.
113.4	107.8	107.8	107.8	105.6	<u>გ</u>	98	93.6	93.6	93.6	87.8	86.2	86.2	81.6	81.6	78.8	77.4	76.8	76.4	76.4	74.2	73.2	72.4	72.4	70.4	8.69	69.4	69.2	68.2	67.2	67	67	67
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ALIGNMENTS

61 CGTTTCGGCGCCAATGAGTTCCTGGGCGCGCGTATTGGTATGGCGATGGTGTTCCCGAG 120 cerrresceceatreatrecrescecececarinsransecariserations 120 121 CTTGGTGAACGGCTACGACGTGGCCGCCATGGCTGCGGGGGAAATGCCAATGTGGTC 180 9 9 1 crcareccarcrececerrecerrecerreceaererrecreerrecreerreceaere Sequence 9, Application US/10450055
Publication No. US20040043953A1
GENERAL INFORMATION No. US20040043953A1
APPLICANT: BASF Aktiengesellschaft
TITLE OF INVENITION: No. US20040043953A1el genes of Corynebacterium
FILE REFERENCE: 936_200
CURRENT APPLICATION NUMBER: US/10/450,055
CURRENT FILING DATE: 2003-06-10
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Vers. 2.0 DB 16; Length 1527; ·; Indels Query Match 100.0%; Score 1527; Best Local Similarity 100.0%; Pred. No. 0; Matches 1527; Conservative 0; Mismatches TYPE: DNA ORGANISM: Corynebacterium glutamicum δ

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Db 1201 TGGGACCAAGGCTGAAGGATGCTTCCAATGTGGATATCTTGATGCACTTGGACA [260] Qy 1261 AGTAAACCTCCAACGGCACGTTTAACCCGCTGAAGGAGGGATGAAGTCAAAGC [320] Db 1261 AGTAAACCTCCAACGGCACTTTAACCCGCTGAAGAAGCAGGGCGATGAAGTCAAAGC [320] Qy 1321 AGGGGAGCTGCTGTGAATTCGATATTGATGCCATTAAGGCTGCAGGTTATGAGGTAAC [380] Db 1321 AGGGGAGCTGCTGTGAATTCGATATTGATGCCATTAAGGCTGCAGGTTATGAGGTAAC [380] Oy 1381 CACGCGATTGTTGTAATTACAAGAAAACCGGACTGCAGGTTATGAGGTTAGG [440] Db 1381 CACGCGATTGTTGTTATACAAGAAAACCGGACTGCAGGTTATGGGTTTTGGG [440] Db 141 CGAAATTGAAGTTGAATTACAAGAAAACCGGACCTGTAAACACTTACGGTTTGGG [440] Oy 141 CGAAATTGAAGCGGAGCCAACCTGCTCAACGTCGCAAAGAACCCGACCACAAC [500] Oy 1501 ACCATAAGTTGAAACCTTGATTCG [527] Db 1501 ACCATAAGTTGAAACCTTGAGTTCG [527]	RESULG. Parameter Application US/0978626 Sequence Application US/0978626 Sequence Application US/0978626 Sequence Application Now US2000197605A Publication Now US2000197605A Publication Now US2000197605A Publication Now US2000197605A Publication Now US2000197605A Publication Now US2000197605A Application Now US2000197605A Application Now US2000197605A Application Now US2000197605A Application Now US2000197605A Application Now US2000197605A Application Now US2000197605A Application Now US2000197605A Application Now US2000197605A Application Now US2000197605A Application Now US2000197605A Application Now US2000197605A Application Now US200019760A Applicati
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Db 2810067 AGTAAACCTCAACGGCACGCACTTAAACCCCTGAAGAAGCAGGGCCATGAAGTCAAAGC 2810008 Qy 1321 AGGGGAGCTGCTGTGTGAATTCGATATTGATGCCATTAAGGCTGCAGGTAATGAGTAAC 1380 Db 2810007 AGGGGAGCTGCTGTGAATTCGATATTGATGCCATTAAGGCTGCAGGTTATGAGGTAAC 2809948 Qy 1381 CACGCGATTGTTGTTTACAATTACAAGAAACCTGTAAACACTTACGGTTATGAGGTAAC 2809988 Qy 1441 CGAAATTGAAGCGGAGCCAACGCTCGAACGACCTGTAAACACTTACGGTTGGG 2809888 Qy 1501 ACCATAAGTTGAAGCGGAGCCAACGTCGCTCAAAGAAAGA	RESULT 3 US-09-738-626-2904 i Sequence 2904, Application US/09738626 i Publication No. US20020197605A1 i GENERAL INFORMATION: APPLICANT: MAKAGAMA, SATOSHI APPLICANT: MAKAGAMA, SATOSHI APPLICANT: ANDO, SEIKO APPLICANT: ANDO, SEIKO APPLICANT: TATELEH, MIKIRO APPLICANT: TATELEH, WACKO APPLICANT: TATELEH, WACKO APPLICANT: TATELEH, WACKO APPLICANT: SENOH, AKHHIRO APPLICANT: SENOH, AKHIRO APPLICANT: SENOH, AKHIRO APPLICANT: SENOH, SEIKO APPLICANT: SENOH, SE	PRIOR APPLICATION NUMBER: JP 00/280988
Db 2811147 CCTGTTTGGTTTTGCCCAAGCCGGTTACCAGGGCACCGTGCTTCCTGTGCTGGT 2811088 Qy 241 GGTTTCTTGGATTCTGCCAACGATCGAGAGCTTCCTCCACAGGCTTCCTGGTCTGGT 2811088 Db 2811087 GGTTTCTTGGATTCTGGCAACGATCGAGAGCTTCCTGCACAGGGCACTGC 300 2811087 GGTTTCTTGGATTCTGGCAACGATCGAGAGATTCCTTACAGGGCACTGC 2811028 Qy 301 AGACTTCCTGATCACTCCAGTGCTGAGATTCCTGCACAGAGCACTCAAGGGCACTGC 2810968 Db 2811027 AGACTTCCTGATCACTCGAGGGTGGCTGAGTGCTCACCGGATTCCTTACATTCATCGC 2810968 Qy 361 CATTGGCCCAGCAATGCGCTGGCTGGCTGCTCACCGGATTCCTTACATTCATCGC 2810908 Qy 421 TGATTTCGGTGGTGGTGGGTGGTGGTGGCTGGCTCACGGTCTACAGGGACTTTA 2810908 Qy 421 TGATTTCGGTGGTGGGGGTGGTGGTTGCTGGTCTACTCGTCATTA 2810908 Db 2810967 CATTGGCCCAGCAATGCGCTGGGTGTGTGTGTGTGTGTCTACAGGGACTTTA 2810908 Qy 421 TGATTTCGGTGGTCCAGTCGCTGCTCTTCGGTCTACTCGTCAT 480 2810907 TGATTTCGGTGGTCCAGTCGGTCTTCGGTCTTACTCGTCAT 2810818	QY 481 CACTGGTCGCACCAGTCCTTCCGGCAATTGAGCTGGAGCTTTAACCAGGGTGGATC 540 Db 2810847 [0-0 0-0 0-0 0-0 0-0 0-0 0-0

Db 1800 AGGGAGCTGCTGTGTGATTTCGATATTGATGCCATTAAGGCTGAAGCTATGGGTAAC 1859 Qy	RESULT 4 US-09-974-300-829 j Sequence 829, Application US/09974300 j Patent No. US20020146721A1 GENERAL INFORMATION: APPLICANT: Berka, Randy M. APPLICANT: Clausen, Ib Groth TITLE OF INVENTION: Methods For Monitoring Multiple Gene TITLE OF INVENTION: Expression FILE REFRENCE: 10085.500-US CURRENT PELLOATION NUMBER: US/09/974,300 CURRENT PELLOATION NUMBER: 09/680,598 PRIOR PELLOATION NUMBER: 09/680,598 PRIOR FILING DATE: 2000-10-06 PRIOR FILING DATE: 2001-10-06 PRIOR FILING DATE: 2001-3-27 NUMBER OF SEQ ID NOS: 8481 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 829 LENGTH: 975 TENGTH: 975 TENGTH: 975 US-09-974-300-829	Query Match Best Local S Matches 437 2 2			As a cartectearcactecargereacg
	481 0 960 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	841 GGTCATGTTCTTGGTGTGTGCAGTTGTTACCTTCTTCATCGCATTCGGCGCAGCGATTGC 900 1320 GGTCATGTTCTTGGTGTGCAGTTGTTACCTTCTTCATCGCCATTCGGCGCAGCGATTGC 137 901 TTATGGCCTTTACTTGGTTCGCCGCAACGCAGCATTGATCCAGATCCACTGCTCC 960 1380 TTATGGCCTTTACTTGGTTCGCCGCAACGGCAGCATTGATCCAGATGCACCGCTGCTCC 960 1380 TTATGGCCTTTACTTGGTTCGCCGCAACGGCAGCATTGATCCAGATGCAACCGCTGCTCC 960	Oy 961 AGTGCCTGCAGGAACGACGAAGCCGAAAGCCCGGCAGAATTTTCAAACGATTC 1020 Db 1440 AGTGCCTGCAGGAACGACCACACAGCCGAGAATTTTTCAAACGATTC 1499 Oy 1021 CACATCATCAAGCACCTTTGACCGGTGAAGCATTTCCACTGAGCATGC 1080 Db 1500 CACATCATCAGGACCTTTGACCGGTGAAGCTATTGCACTGAGCGATGC 1080 Db 1500 CACATCATCAGGCACCTTTGACCGGTGAAGCTATTGCACTGAGCGTCAGCGATGC 1559	OY 1081 CATGITTGCCAGGGAAAGCTTGGCTCGGCGTTGCCATCGTCCCAACCAA	OY 1201 TCGCACCAAGGCTGAGGATGTCCAATGTGGATATCTTGATGCTTTCGACAC 1260

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ATTATGATGTTAAACTTAACACAGAGGGGGTACGATGGTACCGATGTTATTACCAGCC 2089
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                                                                                                                                                                                                                                 1910 GATTGGTTGGGACAAGGATACAAGCAATTTACGCTTTTAGTCCAATTATCGCAGGGTTA
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                                                                                                                Length 5840;
                                                                                                      Score 151.2; DB 9;
Pred. No. 8.5e-36;
0; Mismatches 533;
            ; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-070-927A-31
                                                                                                      9.9%;
                                                                                                                                                                       Conservative
                                                                                                                                   Similarity
                                                                                                                                   Best Local Sim
Matches 525;
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                                                                      535
                                                                                                                                                                                GGATCCITCATCTTCGCAACGGCATCTATGGCTAATATCGCCCAGGGTGCGGCATGTTTG 595
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GAACAATTCGCCGTACTGGGCGGACTGTTATACGGAGGGCTTTACGCCGCTCTCGTCATT 525
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COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-MAy-2000
CLASSIFICATION: CURROWN>
PRIOR APPLICATION: CURROWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05.16
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FILING DATE: 1997-05-06
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FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 40,302
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Patent No. US20020120116A1
GENERAL INFORMATION:
APPLICANT: Charles A. Kunsch
Patrick J. Dillon
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SEQUENCE CHARACTERISTICS:
LENGTH: 5840 base pairs
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STRANDEDNESS: double
TOPOLOGY: linear
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COMPUTER READABLE FORM:
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Mismatches 536;
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Pred. No. 5.4e-31;
                                                                                                                                                 Sequence 3599, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
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48.3%;
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Best Local Similarity 48.3
Matches 539; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Pater
SEQ ID NO 3599
LENGTH: 3037
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     2789 GAATTATCAGTGAAACAAGGTGATTCTGTTAAAAAAGGAGATTTGCTAGTTACTTTTGAT 2848
                                        ATTGATGCCATTAAGGCTGCAGGTTATGAGGTAACCACGCCGATTGTTTGGAATTAC 1405
                                                                        2849 ATTGCTGCCATTAAAGAAGCTGGTTATCCGGTAGTTACACCGATTGTGGTAACGAATACG 2908
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APPLICANT: Berks. Randy M.
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REPERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-03-27
PRIOR FILING DATE: 2001-03-27
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Pred. No. 1e-31;
0; Mismatches 273;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 685
                                                                                                                                                                                                                            Sequence 685, Application US/09974300 Patent No. US20020146721A1 GENERAL INFORMATION:
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Best Local Similarity 53.2%;
Matches 314; Conservative
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US-09-974-300-685
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APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and applications
FILE REFERENCE: 344 702 - US
CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT PILING DATE: 2003-03-27
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
746 ATCGGTGGCGCTTTGATTGCACTCTTTAATATCAAGGCAGTTGCGTTGGG
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                                                                                 1278 TTATGTA------Gradertrcaaadarccadcrdarcradadaa
                        1218 CGAATTCTGGTGGGTAGTTATCGCAATCGTTATCAGCTTCATCCTTGGTTTCATCTTAAC
                                                   CTTGGTTCGCCGCAACGGCAGTTGATCCAGATGCAACCGCTGCTCCAGTGCCTGCAGG
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US-10-398-21-9/c
| Sequence 9, Application US/10398221
| Publication No. US20040018514A1
| GENERAL INFORMATION:
| APPLICANT: GLASER, Pilippe
| TITLE OF INVENTION: Listeria innocua, genome and applications
| TITLE REFERENCE: 344 702 - US
| CURRENT APPLICATION NUMBER: US/10/398,221
| CURRENT FILING DATE: 2003-03-27
| PRIOR FILING DATE: 2001-10-04
| PRIOR PLING DATE: 2001-10-04
| PRIOR PLING DATE: 2001-10-04
| PRIOR FILING DATE: 2001-10-04
| NUMBER OF SEQ ID NOS: 4025
| SOFTWARE: Patentin version 3.0
| SEQ ID NO 9
| LINGTHE SEATOR
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48.2%; Pred. No. 1.3e-29;
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NAME/KEY: misc feature

LOCATION: (1)...(end)

OTHER INFORMATION: n can be any nucleotide: a, US-10-398-221-9
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ORGANISM: Listeria innocua
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Best Local Similarity 48.2
Matches 537; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  29367 cagacetrakanekadegangcarriricarcederecaerriedaaaangereraeearriratee
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Pred. No. 2.6e-28;
0; Mismatches 619; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29715 TGATTACAGATGCAAAAGAAGCTAAACTAGAAG 29747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1425 ACACTTACGGTTTGGGCGAAATTGAAGCGGGAG 1457
          29268 CTGAAGCAGTTGTAGAAGAAACTAACGTAA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 47.1%;
Matches 575; Conservative
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US-10-474-776-160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9034 cacidaaaaaaccarircarcarcargaaccrgrarcgcaggrgcrgriggrggaggaarcarrg 29093
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                                                                                                                                                                                                                                                                             publication US/10398221

publication No. US20040018514A1

publication No. US20040018514A1

general INFORMATION:

APPLICANT: KUNST. Frederik

APPLICANT: GLASER, Philippe

ITLE OF INVENTION: Listeria innocua, genome and applications

FILE REFERENCE: 344 702 - US

CURRENT FILING DATE: 2003-03-27

PRIOR PILING DATE: 2003-03-27

PRIOR PLING DATE: 2001-10-04

PRIOR PLING DATE: 2001-10-04

PRIOR PLING DATE: 2001-10-04

NUMBER OF SEQ ID NOS: 4025

SOFTWARE: PatentIn version 3.0

SSQ ID NO 2058

LENGTH: 3011208

TYPE: DNA
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48.2%; Pred. No. 2.6e-29;
tive 0; Mismatches 534; Indels
                    239891 TGATTACAGATGCAAAGAGCTAAACTAGAAG 239859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Listeria innocua
US-10-398-221-2058
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Publication No. US20020033233A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                 COMPUTER TEADABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDGS version 6.2
SOFTWARE: ASCII Text CURRENT APPLICATION NUMBER: US/08/961,527
APPLICATION NUMBER: US/08/961,527
FLING DATE:
FLING DATE:
APPLICATION NUMBER:
FILING DATE:
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APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFRENCE/DOCKET NUMBER: PB34(
TELECOMMUNICATION INPORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 3895 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                          STATE: Maryland
COUNTRY: USA
ZIP: 20850
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8.3%; Score 126.6; DB 8;
Best Local Similarity 47.1%; Pred. No. 3.4e-28;
Matches 575; Conservative 0; Mismatches 619; 487 604 셤

RESULT 11 US-08-961-527-201/c ; Sequence 201, Application US/08961527

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Pred. No. 3.4e-28;
0; Mismatches 619;
                                                                                                                                                                                                                                                                  NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB340P1D1
                      SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/158,844
FILING DATE: 03-Jun-2002
CLASSIFICATION: <Unknown>
                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/961,527
                                                                                                                                                                                                  60/029,960
                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 201:
SYSTEM: Windows
                                                                                                                                                                           FILING DATE: 1997-10-30
APPLICATION NUMBER: US 6
FILING DATE: 1996-10-31
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3895 base pairs
                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 201:
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
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ilarity 47.1%;
Conservative
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Best Local Similarity
Matches 575; Conserv
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MEDIUM TYPE: CD-R
COMPUTER: Dell Latitude Pentium 3
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TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Human Genome Scier
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
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                                                                                                                                                                                                                                                                                              Length 1884;
                                                                                                                                                                                                                                                                                      Score 113.4; DB 9;
Pred. No. 3.3e-24;
0; Mismatches 601;
                      FastSEQ for Windows Version 4.0
                                                                                           TYPE: DNA ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 46.8%;
Matches 560; Conservative
                                                                                                                                                                                                        ; LOCATION: (1)...(1884)
US-09-815-242-9369
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APPLICANT: Onlsen, Kari L.
APPLICANT: Onlsen, Kari L.
APPLICANT: Onlsen, Kari L.
APPLICANT: Syskind, Judith W.
APPLICANT: Mall, Daniel
APPLICANT: Mall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Detail 11A
CURRENT APPLICANTON NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/204,848
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-12-22
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Patent No. US20020061569A1
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
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CITY: Rockville
STATE: Maryland
COUNTRY: USA
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TITLE OF INVENTION: NOVEL STREPTOCOCCUS PNEUMONIAE OPEN READING FRAMES ENCODING POLYE
TITLE OF INVENTION: ANTIGENS AND USES THEREOF
FILE REFERENCE: AM100649-PCT
CURRENT APPLICATION NUMBER: US/10/474,776
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 752
SOFTWARE: Patentin version 3.1
SEQ ID NO 152
LENGTH: 1185
                                                                                                                                                                                                                                                                                                                                                                            1286 AACCCGCTGAAGAAGCAGGGCGATGAAGTCAAAGCAGGGGAGCTGCTGTGTGAATTCGAT 1345
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                                           TCGGGCGTTGCCATCGTCCCAACCAAGGGGCAGTTAGTTTCTCCGGTGAGGATT
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Pred. No. 1.5e-22;
0; Mismatches 597;
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US-10-474-776-152
Sequence 152, Application US/10474776
Publication No. US20040110181A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Streptococcus pneumoniae
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al Similarity 46.6%;
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Best Local Similarity
Matches 552; Conserv
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                                                                                                                                                                                APPLICATE.

RILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brockes, A. Anders
NAME: Brockes, A. Anders
REGISTRATION NUMBER: 96,373
REFERENCE/DOCKET NUMBER: PB340P1
TELEPCOMMUNICATION INFORMATION:
TELEPCOMMUNICATION 1309-8512
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
ILENCTH: 9769 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
"TOPOLOGY: linear
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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BU345319 BQ988486 BQ986937 CF069882 BE998413

EST48225

QGF3a03.y QGF8003.y Drosophil Tetraodon

Drosophil Petraodon PUHEW79TB SGP154437 EST429680 EST-Conti

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Title:

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PUBERGÉTD ZM 0.6_1.0_KB Zea mays genomic clone ZMMBTa035K11,
BZ685850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zea mays
Sam mays
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="ZMMBTa035K11"
/clone_lb="ZM_0.6_1.0 KB"
/note="Vector: pCK4-TOPO, Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Contact: Cathy Whitelaw
                                                                                                                                             BQ993574 (BQ993574 (BQ991717 (BQ991717 (BQ9917 (BQ9917 (BQ9917 (BQ9917 (BQ9917 (BQ9917 (BQ9917 (BQ9917 (BQ9918 (BB997957 (BB9917 (BQ9918 (BB9917 (BG9918 (BB9917 (BG9918 (BB9917 (BG9918 (BB9917 (BG9918 (BB9917 (BG9918 (BB9917 (BG9918 (BB9917 (BG9918 (BB9917 (BG9918 (BB9917 (BG9918 (BB9917 (BG9918 (BG9917 (BG9918 (BG9917 (BG9918 (BG9917 (BG9918 (BG9917 (BG9918 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG9917 (BG99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Zea mays"
/mol_type="genomic DNA"
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BU345319
BU345319
BQ9986937
BQ991717
BQ991717
BQ998734
BQ998738
BQ998738
BQ99808
CNS006U0
CNS008CW
                                                                                                                                                                                                                                                                                                                        CNS03H6V
CC366418
CK895185
BE997957
CF753589
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1. .917
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Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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Class: sheared ends.
BZ685850.1
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BZ685850/c
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VERSION
KEYWORDS
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ORGANISM
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JOURNAL
COMMENT
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  ORIGIN
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                                                                                                                      October 30, 2004, 13:44:46; Search time 4437 Seconds (without alignments) 12540.787 Million cell updates/sec
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EST429681
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CK159613
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CD442889 ]
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      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                 32822875 seqs, 18219865908 residues
                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
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CL675911
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CL661694
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Oa splbn 04M09 M13reverse Sheep spleen\brain pSport1 library Ovis aries cbNa clone Oa_splbn_04M09 5', mRNA sequence.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                    80
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                                                                                                          Length 750;
                                                                                                                                                                    Indels
                                                                                                       Score 92.6; DB 9;
Pred. No. 5.5e-15;
0; Mismatches 194;
                        /note="Vector: pEpifos-5 Fosmid
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Veterinary Blomedical Sciences
University of Edinburgh
Summerhall Square, Edinburgh, EH9 1Q
Email: j.hopkins@ed.ac.uk
Plate: 04 row: M column: 09
Seq primer: Ml3reverse
High quality sequence stort: 15
High quality sequence stop: 547.
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1 (bases 1 to 770)
Gossner,A. and Hopkins,J.
Ovine spleen\brain cDNA library
Unpublished (2004)
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var. California"
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illarity 53.9%;
Conservative 0
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                                             106 GCCGTTGGTGATCACCGGCATGCACCACATGTTCCTCGCCGTGGACCTGCAGCTTATTTC 47
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/mol_type="genomic DNA"
/strain="California"
/db xref="taxon:54126"
/clone_lib="Nixed stage fosmid library of P. pacificus
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Pristionchus pacificus
Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Roodiplogasterida; Pristionchus.

1 (bases 1 to 750)
Grinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppabB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  469 ACCAATCGTCATCACTGGTCTGCACCAGTCCTTCCCGCCAATTGAGCTGGAGC---TGTT
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This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: I7
Class: fosmid ends.
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Max.Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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P037-3-E04.za Ppa EcoRI BAC Library Pristionchus pacificus genomic, genomic, survey sequence.
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Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
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                                                                              /mol_type="genomic_DNA"
/strain="california"
/db_xrre="taxon:54126"
/clone_lib=whixed_stage fosmid library of P. pacificus
var. California"
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/strain="california"
/db xref="texon:54126"
/clone lib="texon:54126"
/clone lib="texon:54126"
/note="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC
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Neodiplogasteridae, Pristionchus.
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Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Fax: 00497071601391
Email: ralf.sommer@tuebingen.mpg.de
                                                          pacificus"
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Pred. No. 2.3e-09;
                                                            organism="Pristionchus"
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Best Local Similarity 55.0%;
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PRI0129d_H09 - PRI0129d.B21 (861) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic
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(Léases: Lto 861)

S frinivasan, J.; Otto, G W., Kahlow, U., Geisler, R. and Sommer, R.J.

AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus

L Nucleic Acids Res. 32 (1), D421-D422 (2004)

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Fax: 00497071601371
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                                                                                                                                                                                           181 CCTGTTTGGT-----TTAGATGTTGCCCAAGCCGGTTACCAGGCCACGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 TCCTGTGCTGGTGTTTCTTGGATTCTGGCAACGATCGAGAAGTTCCTGCACAAGCGACT
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                                                                                                                  13; Gaps
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/clone_lib="Sheep spleen\brain pSport1 library"
                                                                     Length 770;
                                                                                                                Indels
                                                                 Score 80.8; DB 7; Pred. No. 1.4e-11; 0; Mismatches 242;
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This library was generated at Caltech,
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
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CL657583.1 GI:50139334
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Pristionchus pacificus
                                                            Query Match 5.3%;
Best Local Similarity 50.4%;
Matches 259; Conservative
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TITLE
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CL657583
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Query ORIGIN

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P. pacificus
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This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.

Seq primer: T7
Class: formid ends.

1. 788
/organise="Pristionchus pacificus"
/mol type="genomic DNA"
/strain="California"
/db xref="texxon:54126"
/db xref="texxon:54126"
/db xref="texxon:54126"
/db xref="texxon:54126"
/db xref="texxon:54126"
/done_lib="Mixed stage fosmid library of P. pacificus.
/actor: pBpifos-5 Fosmid vector"
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/culTivar="barke"
/sub_species="vulgare"
/db_xref="teaxon:112509"
/clone="HY021241"
/tissub_type="developing caryopsis (3.-15.DAP)"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 62; DB 9; Length 788
Pred. No. 3.8e-06;
0; Mismatches 125; Indels
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ilarity 52.3%;
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Matches 137; Conserv
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PRIO162a D06_2 - PRIO162a.BR (788) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic
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Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 788)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppaDB: an AcedB database for the nematode satellite organism
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                                                                                                                                                                      Length 1412;
                                                                                                                                                                  Score 63.2; DB 9; Length 1
Pred. No. 2.1e-06;
0; Mismatches 308; Indels
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Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
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Email: ralf.sommer@tuebingen.mpg.de
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Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena,
sequenced at Vancouver, Canada.
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Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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Srimivasan, J., Otto, G.W., Kahlow, U., Geisle:
AppadB: an AcedB database for the nematode s
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
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/note="Wetcr: plasmid pBK-CWV, Site 1: EcoRI; Site 2: Xho1; mRNA was made from developing caryopsis (3.-15_DAP) of spring barley variety 'Barke', a high quality malting variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb Sequence trimming: Vector sequences and sequence ends were trimmed from the 5'-and 3'-end until a 50 bp window contains less than two ambiguities. The maximum length was set to 700 bp"
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.

(bases 1 to 1328)
Spencer, D.H., Kaymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of
Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
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University of Washington
Box 352145, Seattle, WA 98105-2145,
Tel: 2062216954
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Email: craymond
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Matches 163
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CL695497
PRI016c_C08_2 - PRI016c.BR (763) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic CL699497

DEFINITION

ACCESSION

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                                                                                                                            Neodiplogasteridae; Pristionchus.

1 (Sontact: Sommer RJ (1), D421-D422 (2004)
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/dlone lib="Mixed stage fosmid library of
var. California"
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Max-Planck-Institute for Developmental Biology
Max-planck-Institute for Developmental Biology
Tel: 00497071601371

    763
/organism="Pristionchus pacificus"

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Pred. No. 0.12;
); Mismatches 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 00499/071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech,
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
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/strain="California"
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Pristionchus pacificus
Pristionchus pacificus
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Best Local Similarity 45.6%;
Matches 247; Conservative
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DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE

RESULT 11 T03017/c

ORGANISM

REFERENCE AUTHORS MEDLINE PUBMED

COMMENT

JOURNAL

TITLE

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/clome lib="pistil, 1 DPA, no treatment, cv Optic, EBpi01"
/note="Vector: pSPORT1; Site_1: Sal I; Site_2: Not I;
Non-normalised library, directionally cloned into pSPORT1.
Porlived from pistils dissected from developing grains (24 hours post anthesis) in glasshouse grown barley plants.
Developed as part of the barley transcriptome resources of BassRC/SERAD funded cereal IGF (Investigating Gene
            EST.
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
Pooideae; Triticeae; Hordeum.
Liliopsida; Nordeum.
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PRI013c_B10 - PRI013c.B21 (791) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
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                                                                                                                                                                                            Cardle, L.,
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                                                                                                                                                                             Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Card Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R. Development of Barley Transcriptome Resources Unpublished (2001)
On Nov 21, 2001 this sequence version replaced gi:17031891. Contact: Waugh R, Marshall DF Genome Dynamics/Computational Biology
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/organism="Hordeum vulgare subsp. vulgare"
/mol_type="maNA"
/mol_type="maNA"
/ullivar="Optio"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="RBpiol S0002 B17"
/tissue_type="pistil"
/dev_stage="1 DPA"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or over
                                                                                                                                                                                                                                                                                                                                                  Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UX
Tel: 00 44 1382 562731
Fax: 00 44 1382 562736
Ramil: est@scri.sari.ac.uk
All sequence has a Phred quality score of 20 est primer: M13 reverse
Location/Qualifiers
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               KEYWORDS
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                                                                                                                                                                                       FB20C8 Fetal brain, Stratagene Homo sapiens cDNA clone FB20C8, mRNA
                                                                                                                                                                             EST 14-FEB-1997
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EBpi01 SQ002_B17_R pistil, 1 DPA, no treatment, cv Optic, EBpi01
Hordeum vulgare subsp. vulgare cDNA clone EBpi01_SQ002_B17 5', mRNA
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/note="Vector: Lambda ZAP II, The FB library (catalog #937201, Stratagene) was constructed by directional clouding and oligo d(T)-priming in Lambda ZAP II phage utilizing mRNA from a 17 week human fetus (total brain)."
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                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 473)

Khan, A.S., Wilcox, A.S., Polymeropoulos, M.H., Hopkins, J.A., Stevens, T.J., Robinson, M., Orpana, A.K. and Sikela, J.M..
Single pass sequencing and physical and genetic mapping of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 TCTGGTGGAAGAGGGTGCGCAGGTAAGCGCAACCGAATCGAAAATGGATCTGGA 156
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Contact: Sikela JM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Pharmacology
University of Colorado Health Sciences Center
Box C236, 4200 B. 9th Ave, Denver CO 80262-0236
Tel: 3032708637
Fax: 30327070997
                                                                                                                                                                             mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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/db_xref="GDB:D082785E"
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                                                                                                                                                                        473 bp
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Location/Qualifiers
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BM100823.2 GI:21943888
                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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Best Local Similarity
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SOUTH

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FEATURES

RESULT 12 BM100823/c

8

DEFINITION

ACCESSION VERSION

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Gaps

695

us-09-604-231-1.rst

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EST:
Triticum aestivum (bread wheat)

Triticum aestivum

Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Poaceae;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Triticum.

E (bases 1 to 869)

S Allard, F. (crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,

Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilson, D.,

Penniket, C., Roach, J.L. and Sarhan, F.

Punctional Genomics of Abiotic Stress In Wheat and Canola Crops

Contact: Wm L Crosby
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1 (bases 1 to 785)
Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA linear EST 05-DEC-2 Talt5 Triticum aestivum cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRN4"
/cullivar="mRN2"
/db_xref="taxon:4577"
/tissue_type="Endosperm of 7-23DAP"
/clone_lib="Endosperm 4"
/note="Vector: pBluesGript SK-; Site_1: EcoRI; Site_2:
XhoI=
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                                                                                                                                                  Necestrugy.v. Sequencing of the maize endosperm ESTs Unpublished (2002) Contact: Lai, Jinsheng Dr. Joachim Messing's lab Waksman Institute, Rutgers University 190 Frelinghuysen Rd., Piscataway, NJ 08854, USA Tel: 732-445-3801 Fax: 732-445-5735 Email: jlai@waksman.rutgers.edu Seq primer: T3
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0.45;
ches 156;
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46.9%; Pred. No. 0.45;
iive 0; Mismatches
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FGAS040564 Triticum aestivum FGAS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Zea mays"
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Matches 138; Conservative
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CK159167.1 GI:
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.

1 (bases 1 to 791)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J. AppabBs an AcedB database for the nematode satellite organism Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
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/dlone lib=Mxxed stage fosmid library of
var. California"
/note="Vector: pEpifos-5 Fosmid vector"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 00497071601371
Fax: 00497071601438
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, sequenced at Vancouver, Canada.
                                                                                                                                                                                                                                                                                                                                                                                                                Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45.4; DB 9; I
Pred. No. 0.23;
0; Mismatches 161;
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Location/Qualifiers
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Pristionchus pacificus
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Similarity 46.9%;
42; Conservative (
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CD443326/c
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RA Gosmann A., Hathmacher K., Kraemer R., Lihke B.,
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RA Tauch A.,
Rey D.A., Rueckert C., Rupp O., Sahm H., Wendisch V.F., Wiegraebe I.,
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                                                                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Phosphotransferase system IIC components, glucose/maltose/N-acetylglucosamine-specific (EC 2.7.1.69) (ENZYME II SUCROSE PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name-ptss; OrderedLocusNames=Cg12642, cg2925; Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacterineae; Corynebacterineae; Corynebacterineae; Corynebacterineae; Corynebacterineae; Corynebacterineae; Corynebacterium.
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Burkovski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat L.,
Goesmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
McHardy A.C., Mayer F., Moeckel B., Pfefferle W., Puehler A.,
Feey D.A., Rueckert C., Rupp O., Sahm H., Wendisch V.F., Wiegraebe I.,
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and vitamins.",
a. Biotechnol. 104:5-25(2003).

EMBL; EX927155; CAF21304.1; -.
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Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1718;
                                                                          DB 2; Length 661;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 661 AA; 69148 MW; COESEIC7833B9F74 CRC64;
                                                      COE5E1C7833B9F74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last annotation update)
                                                                         100.0%; Score 2363; DB 2;
100.0%; Pred. No. 3.6e-144;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAR-2004 (TrEMBLrel. 27, Created) 02-MAR-2004 (TrEMBLrel. 27, Last sequence update) 02-MAR-2004 (TrEMBLrel. 27, Last annotation updat ENZYME II SUCROSE PROTEIN (EC 2.7.1.69).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
SEQUENCE TROM N.A.
Pubmed=12948626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   661 AA
TIGRPAMS; TIGRO0830; PTBA; 1.
TIGRPAMS; TIGRO1996; PTS-II-BC-sucr; 1.
PROSITE; PSO1035; PTS_EIIB_CYS; 1.
Complace proteome; Transferase.
SEQUENCE 661 AA: CALL
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                                                                                                 Conservative
                                                                                      Similarity
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                                                                                                 468;
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                                                                                                                                                                                                                                                                                                                                                                                                                 241 SIDAPDWVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEABAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    494 ABFSNDSTIIQAPLTGRAIALSSVSDAMFASGKIGSGVALVPTKGQLVSPVSGKIVVAFP
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                                                                                         1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLFVLVVSWILATIEKFLH
                                                                                                                                      194 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH
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                                               Gaps
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T'Complete genome sequence of Lactobacillus plantarum WCFS1.";
Theo. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
R HSSP: P20166; 1GPR.
R GO; GO:001669: C:membrane; IEA.
GO; GO:0016029; F:protein-N(PI)-phosphohistidine-sugar phosph. . .;
R GO; GO:0016740; F:ranaferase activity; IEA.
GO; GO:0016740; F:transport; IEA.
GO; GO:0016740; F:transport; IEA.
R GO; GO:0016740; F:transport; IEA.
R GO; GO:0016810; F:transport; IEA.
R GO; GO:0010940; P:transport; IEA.
R InterPro; IPR011055; DUP_hybrid_motif.
R InterPro; IPR001352; Ptrans_EIIE.
R InterPro; IPR003352; Ptrans_EIIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=NCIMB 8826 / WCFS1;
MEDLINE=22480296; PubMed=12566566;
Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
Klerebezem M., Boekhorst W., Peters S.A., Sandbrink H.M.,
Fiers M.W. E.J., Stiekem W., Klein Lankhorst R.M., Bron P.A.,
Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing
De Vos W.M., Siezen R.J.;
                                               ;
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661;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
  Length
                                               Indels
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  Score 2363; DB 2;
Pred. No. 3.6e-144;
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01-UTN-2003 (TrEMBLrel. 24, Last sequence up
01-MR-2004 (TrEMBLrel. 26, Last annotation
sucrose PTS, EIIBCA (EC 2.7.1.69).
Name-ptsiECA, OrderedLocusNames=lp_0185;
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                                               0; Mismatches
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       100.0%;
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                                Local Similarity 100.
nes 468; Conservative
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68454 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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324
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651 AA;
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                                                                                                                                                                                                                                                                      VYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGAACLAVFFLAKSEKL
                                                                                                                                                                                       1 MAMVFPSLVNGYDVAATWAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH
                                                                                                                                                                                                    194 MINVLPSLVNGYSVATTMAAGKOVYWNVFGLHVAQAGYQGQVLPVLAVAYLLATLEKFFH
                                                                                                                                                                                                                               KRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL
                                                                                                                                                                                                                                          Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: This is a component of the phosphoenolpyruvate-dependent
                                                                                                                                                                                                                                                                                                               KGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGF
                                                                                                                                                                                                                                                                                                                                                                                                AEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIV
                                                                                                                                                                                                                                                                                                                                                        LGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAE
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pediococcus pentosaceus.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; Pediococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
PTS system, sucrose-specific ILABC component (BIIABC-Scr) (Sucrose-permanse ILABC component) (Phosphotransferase enzyme II, ABC component) (BC 2.7.1.69) (BII-Scr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKKEA--VPAT 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         649
                                                                                                                                                45.0%; Score 1062.5; DB 2; Length 651; 46.7%; Pred. No. 2.7e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | | | | : : : | | | : | | | | | ABLKAANYDPTVMLVVINTANYANVERLKVTINVQAGEQLVALTEPTASSVAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leenhouts K.K.J., Bolhuis A.A., Kok J.J., Venema G.G., "The sucrose and raffinose operons of Pediococcus pentosaceus
                                                                                                                                                                    80; Mismatches 149; Indels
                                                                                                                             68514 MW; CBFB535EDDB73DD6 CRC64;
InterPro; IPR001127; PTS EIIA.
InterPro; IPR010973; PTS III BC_sucr.
Pfam; PF00058; PTS EIIA 1; 1.
Pfam; PF00367; PTS EIIB 1;
ProDom; PF002378; PTS EIIC; 1.
ProDom; P0002248; PTS EIIC; 1.
TGRPAMs; TIGR00830; PTBL; 1.
TIGRPAMs; TIGR00830; PTBL; 1.
TIGRPAMs; TIGR01996; PTS-II-BC-sucr; 1.
PROSITE; PS00371; PTS EIIA; 1.
PROSITE; PS01035; PTS EIIA; 1.
COMplete protecome; Transferase.
SEQUENCE 651 AA; 68514 MW; CBFB535EDDB
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                                                                                                                                                                  Matches 221; Conservative
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                                                                                                                                                          Similarity
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P43470;
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                                                                                                                                                Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Enropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
sugar phosphotransferase system (PTS), a major carbohydrate active—transport system. The IICD domains contain the sugar binding site and the transmembrane channel; the IIA domain contains the primary phosphorylation site (the donor is phosphoryler); IIA transfers it be phosphoryl group to the IIB domain which finally transfers it to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAMVFPSLVNGYDVAATWAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH
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46.7%; Pred. No. 4.9e-60;
iive 78; Mismatches 151; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphocysteine (By similarity).
Phosphohistidine (By similarity)
Phosphohistidine (By similarity)
C87BA09D550A77F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00371; PTS EIIA 1; 1.
PROSITE; PS01035; PTS EIIB CYS; 1.
Phosphorylation; Phosphotransferase system; Sugar transport;
                                                                                                                                                                                                                                                                              protein.
                                                                                                                                                                                                                           histidine + sugar phosphate.
-!- SUBCELIULAR LOCATION: Integral membrane
-!- SIMILARITY: COntains 1 PTS EIIB domain.
-!- SIMILARITY: Contains 1 PTS EIIB domain.
-!- SIMILARITY: Contains 1 PTS EIIB domain.
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TIGRFAMS; TIGR01996; PTS-II-BC-sucr; 1.
TIGRFAMS; TIGR01992; PTS-IIBC-Tre; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, P20166, 1GPR.
InterPro, IPR011055, Dup hybrid motif.
InterPro, IPR011055, Prians BIIB.
InterPro, IPR001395, Prans BIIB.
InterPro, IPR00127, PTS BIIA.
InterPro, IPR010973, PTS EIIA.
InterPro, IPR010973, PTS EIIA.
Fam, PP00358, PTS EIIB 1, Pfam; PF003567, PTS EIIB 1, Pfam; PF003567, PTS EIIB 1, ProDom, PD001243; PTS EIIB, 1.
ProDom, PD001243; PTS EIIB, 1.
ProDom, PD001476, PTS EIIB; 1.
PTGRPAMS; TIGR00826; EIIB 91c; 1.
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                                                     261 KSLTTSAGISAMLGITEPALFGVNLKLKFPFFIGLIASGISSFIIGLHVLSVSMGPAGI 320
                                                                                                                                                     237 LGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAE 296
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NEDINE-99173919; PubMed=10074089;

NEDINE-99173919; PubMed=10074089;

NEDINE-99173919; PubMed=10074089;

NEDINE-99173919; PubMed=10074089;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLCEFDIDAIKAAGYEVTTPIVVSN---YKKTGPVNTYGLGEIEAGANLLNV-AKKE 462
              KGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69636 MW; 250E26F7664D4204 CRC64;
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                                                                                                                                                                                                    :| ::| ::| ::| ::| 321 IGFIAIAPKSIPSFWMGAIISFVIAFVGTYLYGKKAMK-
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TIGREAMS; TIGRO1996; PTS-II-BC-sucr;
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PROSITE; PS01035; PTS_EIIB_CYS;
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                                                                                                   AEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIV 356
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Dudez A.M., Chaillou S., Hissler L., Stentz R.,
Champomier-Verges M.C., Alpert C.A., Zagorec M.;
Champomier and genetic map of the Lactobacillus sakei 23K chromosome.";
Microbiology 148:421-431(2002).
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                                                                                                                                              VAPPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDI
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                                                                                                                                                                                                                                                                                                                                                                                                                          417 DAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANL--LNVAKKEAVPAT
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Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF401046; AAK92528.1; -.
HSSP; P45618; 2GPR.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
10-DR-2004 (TrEMBLrel. 26, Last annotation update)
Sucrose-specific enzyme II of the PTS (Fragment).
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Best Local Similarity
Matches 211; Conserv
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               121 VYSPIVITGIHQSFPPIELELFNQ-----GGSFIFATASMANIAQGAACLAVFFLAKSB 174
                                                                                         175 KLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAA 234
                                                                                                     294
                                                                                                                                                                                                           540
                                                                                                                                                                                                                                        295 AEAEAPAEFSNDSTIIQ-----APLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQ 346
                                                                                                                                                                                                                           LVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNINGTHFNPLKKQGDEVK 406
                                                                  314 FYSAIVVTGLHQSFPALETMLITNYQHSGIGGDFIFPVAACANMAQAGATFALLFVTKNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDILINE=89123027; PubWed=2536656; Sato Y., Poy F., Jacobson G.R., Kuramitsu H.K.; Accheration and sequence analysis of the scrA gene encoding enzyme IIScr of the Streptococcus mutans phosphoenolpyruvate-dependent
                                                                                                                                                   GFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTK
                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
PTS system, sucrose-specific IIABC component (BIIABC-Scr) (Sucrose-permease IIABC component) (Phosphotransferase enzyme II, ABC component) (BC 2.71.69) (BII-Scr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of Streptococcus mutans UA159, a cariogenic dental pathogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sato Y., Yamamoto Y., Kizaki H., Kuramitsu H.K., "Isolation, characterization and sequence analysis of the scrK gene encoding fructokinase of Streptococcus mutans."; J. Gen. Microbiol. 139:921-927(1993).
                                                                                                                                                                                                                                                                      AGELLCEFDIDAIKAAGYEVTTPIVVSN---YKKTGPVNTYGLGEIEAGANLL 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN-UALS9 / ATCC 700610 / Serotype c;

MEDLINE-22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;

Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,

Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.

Qian Y., Li S., Zhu H., Najar F.Z., Lai H., White J., Roe B.A.,

Ferretti J.J.;
                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              roc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002)
                                                                                                                                                                                                                                                                                                                                                      664 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=scrA; OrderedLocusNames=SMU.1841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sucrose phosphotransferase system.",
J. Bacteriol, 171:263-271(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93329360; PubMed=8336109;
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                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus mutans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=GS-5;
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253
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FUNCTION: This is a component of the phosphoenolpyruvate-dependent sugar phosphotransferase system (PTS), a major carbohydrate active transport system. The ILCD domains contain the sugar binding site and the transmembrane channel; the IIA domain contains the primary phosphorylation site (the donor is phospho-HPr); IIA transfers its phosphoryl group to the IIB domain which finally transfers it to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAMVFPSLVNGYDVAATMAAGEMP-----MWSLFGLDVAQAGYQGTVLPVLVVSWILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 GGLLFGLVYSPIVITGLHQSFPPIBLEL---FNQG---GSFIFATASMANIAQGAACLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: Protein N-phosphohistidine + sugar = protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00371; PTS BIRA 1; 1.
PROSITE; PS01035; PTS BIRA 1; 1.
Complete proteome; Phosphorylation; Phosphotransferase system; Sugar transport; Transferase; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphohistidine (By similarity)
Phosphohistidine (By similarity)
809B63B32281A9A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89; Mismatches 156; Indels
                                                                                                                                                                                                   histidine + sugar phosphate.
-- SUBCELLUIAR LOCATION: Integral membrane protein.
-- SIMILARITY: Contains 1 PTS EIIA domain.
-- SIMILARITY: Contains 1 PTS EIIB domain.
-- SIMILARITY: Contains 1 PTS EIIC domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD002243; FTS EIIA; 1.
ProDom; PD001476; PTS EIIB; 1.
TIGRFAMS; TIGR00826; EIIB glc; 1.
TIGRFAMS; TIGR00830; PTBA; 1.
TIGRFAMS; TIGR01995; PTS-II-ABC-beta; 1.
TIGRFAMS; TIGR01996; PTS-II-BC-sucr; 1.
TIGRFAMS; TIGR01996; PTS-II-BC-sucr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69988 MW;
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349

409

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61 KRLKGTADFLITPVLTLLLTGFLTFIALGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 VYSPIVITGLHQSFPPIELELFNQ-----GGSFIFATASMANIAQGAACLAVFFLAKSE 174
                                                                                                                                                                                                                                                                                235 GFLGVVSIDAPDMVMFLVCAVVTFFIAFGAALAYGLY----LVRRNGSIDPDATAAPVP 289
                                                                                                                                             303 SYSAIVTTGLHQSFPAVETQLLAEYARGRGSGDFIFVTACMANVAQGAATFAIYFLTKNE 362
                                                                                                                                                                                                  KLKGLAGASGVSAVLGITEPALFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAA 234
                                                                                                                                                                                                                         KRLKGTADFLITPVLTLLIGGFLTFIAIGPAMRWYGDVLAHGLQGLYDFGGPVGGLLFGL 120
                                                                                                                    VYSPIVITGLHQSFPPIELELFNQ-----GGSFIFATASMANIAQGAACLAVFFLAKSE 174
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                                                                                                                                                                                                                                                                                                                                                                                      480 AQQEKAEQIIKEDKELHDEVIAAPVSGKAESLKDVNDPVFSTEAMGKGAAMVPSEGTIYS
                                                                                                                                                                                                                                                                                                                                                                                                                                               350 PVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---GGAGKYWDIFGLHVSQTNYQYQVIPVLVAVWLLAFLEKRFH
                                                               243 KWLPSAVDFTFTPLLSIMITGFLTFTIIGPVFKGVSDAITAALVWLYNTTGAFGMGIFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Phosphoenolpyruvate-dependent sugar phosphotransferase system EIIABC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C., Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou R., Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.; "The genome sequence of the probiotic intestinal bacterium lactobacillus johnsonii NCC 533."; Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517 (2004).

Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517 (2004).

Pyruvate, Transferase.
SEQUENCE 647 AA, 69202 MW, 95FA74C533CE9541 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             410 LLCEFDIDAIKAAGYEVITPIVVSNYKKIGPVNTYGLGEIEAGANLLNVAKK 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 914.5; DB 2; Length 647;
; Pred. No. 9.5e-51;
88; Mismatches 160; Indels 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Firmicutes, Lactobacillales, Lactobacillaceae, Lactobacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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        194 MIMTTPAL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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PubMed=14966310;
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                                                      489 VEBAIEEVQ-EIPEEAASAANKAQVTDEVLAAPLAGEAVELITSVNDPVFSSEAMGKGIAI 547
                                                                                                                                                                                            VPIKGQLVSPVSGKIVVAFPSGHAFAVRIKAEDGSNVDILMHIGFDTVNLMGTHFNPLKK 400
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PubMed=1496610.

PubMed=1496610.

Pridenore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,

Pridet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou R.,

Amollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;

Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;

The genome sequence of the probiotic intestinal bacterium actobacilus johnsonin NCC 533.";

Experimental Designation of the probiotic intestinal bacterium actobacilus johnsonin NC 633.";

Experimental Designation of the probiotic intestinal bacterium actobacilus johnsonin NC 3.

Experimental Designation of the probiotic intestinal bacterium actoric proposition phybrid motif.

Experimental Designation of the probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic probiotic prob
                             AVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAP
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Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                os-oul-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
phosphoenolpyruvate-dependent sugar phosphotransferase
sucrose specific.
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ilarity 41.3%; Pred. No. 9.5e-51;
Conservative 88; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      647 AA
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SEQUENCE 647 AA; 69202 MW; 95FA74C53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00371; PTS EIIA 1; 1.
PROSITE; PS01035; PTS_EIIB_CYS; 1.
                                                                                                                  VPAGTTKAEAEAPAEFSNDST---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OrderedLocusNames=LJ0519;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lactobacillus johnsonii
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Best Local Similarity
Matches 195; Conserv
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"Functional and comparative genomic analyses of an operon involved in
fructooligosaccharide utilization by Lactobacillus acidophilus.";

"Funct Soligosaccharide utilization by Lactobacillus acidophilus.";

"Froc. Natl. Acad. Sci. U.S.A. 100.8957-8962(2003).

"RENEL, AY177419; AA038866.1;

"RENEL, AY177419; AA038866.1;

"ROG. GO:001620; C:membrane, IEA.

"ROG. GO:001620; F:protein-N(PI)-phosphohistidine-sugar phosph. .; IEA.

"ROG. GO:000531; F:sugar porter activity; IEA.

"ROG. GO:0005401; P:prosphoenolyptuvate-dependent sugar phospho. .; IEA.

"ROG. GO:0006810; P:transferase activity; IEA.

"ROG. GO:0006810; P:prosphoenolyptuvate-dependent sugar phospho. .; IEA.

"RICEPTO: IPRO1356; Ptrans EIIB.

"InterPro: IPRO1357; PTS_EIIA.

"InterPro: IPRO1358; PTS_EIIA.

"InterPro: IPRO1358; PTS_EIIA.

"InterPro: PRO0358; PTS_EIIA.

"InterPro: PRO0358; PTS_EIIB.

"InterPro: PRO0358; PTS_EIIB.

"InterPro: PRO0358; PTS_EIIB.

"InterPro: PRO0358; PTS_EIIB.

"InterPro: PRO0358; PTS_EIIB.

"InterPro: PRO0358; PTS_EIIB.

"InterPro: PRO0358; PTS_EIIB.

"InterPro: PRO0358; PTS_EIIE.

"InterPro: PRO0358; PTS_EIIE.

"InterPro: PRO0358; PTS_EIIE.

"InterPro: PRO0358; PTS_EIIE.

"InterPro: PRO0358; PTS_EIIE.

"InterPro: PRO0368; PTS_EIIE.

"InterPro: PRO0368; PTS_EIIE.

"InterPro: PRO0368; PTS_EIIE.

"InterPro: PRO0368; PTS_EIIE.

"InterPro: PRO0368; PTS_EIIE.

"InterPro: PRO0368; PTS_EIIE.

"InterPro: PRO0368; PTS_EIIE.

"InterPro: PRO0368; PTS_EIIE.

"InterPro: PRO0368; PTS_EIIE.

"InterPro: PRO0368; PTS_EIIE.

"InterPro: PRO0368; PTS_EIIE.

"InterPro: PRO0368; PTS_EIIE.

"InterPro: PRO0368; PTS_EIIE.

"InterPro: PRO0368; PTS_EIIE.

"InterPro: PRO0368; PTS_EIIE
SYSAIVTTGLHQSFPAVETQLLAEYARGRGSGDFIFVTACMANVAQGAATFAIYFLTKNE 362
                                                                                                                                                              422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    350 PVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGE 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             595
                                                                     175 KLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAA
                                                                                                            235 GFLGVVSIDAPDMVMFLVCAVVTFFIAFGAALAYGLY----LVRRNGSIDPDATAAPVP
                                                                                                                                                                                                                                                                                                                                                                290 AGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVS
                                                                                                                                                                                                                                                                                                                                                                                                           410 LLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKK 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              596 KLGTVDLDAVKKAGYDTTVMTVITNTTSYANVQRIDGVEKKHGDDLIAVTKR 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.1%; Score 901; DB 2; Length 64.40.8%; Pred. No. 7.16-50; Live 81; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
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Last annotation update)
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ProDom; PD002243; PTS BIII; 1.
TIGREAMS; TIGR00830; PTBA; 1.
TIGRFAMS; TIGR01996; PTS-II-BC-sucr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequ
01-MAR.2004 (TrEMBLrel. 26, Last anno
Sucrose PTS transporter (EC 2.7.1.69)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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PROSITE; PS01035; PTS_EIIB_CYS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lactobacillus acidophilus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 40.89
Matches 183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1579;
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PubMed=12847288;
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1 MAMVEPSLVNGYDVAATMAAGEMEMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH 60

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194 MIMTIPGL------GGATKFWDIFGLHVAQTNYQYQVIPVLVAVWVLSIFEKYFH 242
                                                                243 KHLPSAVDFTFTPLLSIMITGFLTFTIIGPVFKGVSDAITNAIVWLYDTTGAFGMGVFKGL 302
                                                                                                                      121 VYSPIVITGLHQSFPPIELELF-----NQGGSFIFATASMANIAQGAACLAVFFLAKS 173
                                                                                                                                                     303 SYSAIVTTGLHQSFPAVETQLLAAFAKNPASSGDFIFVTACMANVAQGAATFAVYFLTKN 352
                                                                                                                                                                                                                                                                                                                                                                        292 -----TTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKG 345
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                                      61 KRLKGTADFLITPVLTLLITGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL
                                                                                                                                                                                                      174 EKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGA
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-V583 / ATCC 700802,
WEDLINE-22550857; PubMed-12663927; DOI=10.1126/science.1080613;
Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R.,
Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
Tettelin H., Dodson R.J., Umayam L.A., Brinksc L.M., Beanan M.J.,
Daugherty S.C., Down R.T., Durkin S.A., Kolonay J.F., Madupu R.,
Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                        AGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAG--
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R GO; GO:0016020; C:membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005321; F:sugar porter activity; IEA.

GO; GO:000531; P:sugar porter activity; IEA.

GO; GO:000531; P:sugar porter activity; IEA.

R GO; GO:000531; P:sugar porter activity; IEA.

R GO; GO:000531; P:sugar porter activity; IEA.

R InterPro; IPR010155; Dup Pybrid motif.

R InterPro; IPR001352; Ptrans EIIA.

R InterPro; IPR00137; PTS EIIA.

R InterPro; IPR00137; PTS EIIA.

R InterPro; IPR00353; PTS EIIA.

R Pfam; PF00358; PTS EIIB.

R Pfam; PF00357; PTS_EIIB.

R Pfam; PF00357; PTS_EIIB.

R Pfam; PF00357; PTS_EIIB.

R Pfam; PF00357; PTS_EIIB.
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Science 299:2071-2074(2003).
EMBL; ARO16833; AAO83060.1; -.
HSSP; P20166; 1CPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterococcus faecalis (Streptococcus faecalis).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KAGELLCEFDIDAIKAAGYEVTTPIVVSN 434
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01-JUN-2003
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DOI=10.1128/JB.183.16.4823-4838.2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234
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                                                                                                                                                                                                                                                                                                                                            KKLPSSIDFTFTPLLSVIITGFLTFTVIGFTMLLLSNGITDAIVMLYNATGFIGMGIFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481 INTNQIANADEPTTVETIVSPLAGEITTLGSVNDFVFSSESIGKGIAIKPNGNTIYSPVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH
                                                                                                                                                                                                                                                                                                                                                                                                     KRLKGTADFLITPVLTLLIGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 TYSLIVWTCLHQSFPAIETQLLSAWTNGIGHGDFIFVVASMANVAQGAATFAIWFLTKNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLIKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 AEAEAPAEFSNDSTI--IQAPLIGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQG--DEVKAGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=scrA; OrderedLocusNames=CAC0423;
Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                       29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIBAGANLLNV 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGTFDSTVITNSGLDDTTMVIVTNSKDYSEVIPITKNIVTEGAALLTI 642
                                                                                                                                                                                                                              643;
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2004 (TrEMBLrel. 28, Last annotation update)
01-007-2004 (TremBLrel. 28, Last annotation update)
01-007-2004 (TremBLrel. 28, Last annotation update)
01-007-2004 (TremBLrel. 28, Last annotation update)
                                                                                                                                                                                                                            DB 2; Length
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                  68532 MW; 752F65D8154AA06C CRC64;
                                                                                                                                                                                                                         35.2%; Score 832.5; DB 2;
39.3%; Pred. No. 1.8e-45;
iive 84; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=ATCC 824;
MEDLINE=20391269; Pubmed=10937490;
Tangney M., Mitchell W.J.;
"Analysis a catabolic operon for sucrose in Clostridium acetobutylicum ATCC 824.";
J. Mol. Microbiol. Biotechnol. 2:71-80(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 627
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  Pfam, PF02378; PTS EIIC; 1.
ProDom; PD001476; Ptrans EIIB; 1.
ProDom; PD00244; PTS EIIA; 1.
TIGRPAMS; TIGR00830; PTBA; 1.
TIGRPAMS; TIGR01996; PTS-II-BC-sucr; 1.
PROSITE; PS00371; PTS EIIA 1; 1.
PROSITE; PS01035; PTS_EIIB_CYS; 1.
Complete protecome; Plasmid.
SEQUENCE 643 AA; 68532 MW; 752F65D8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-:
MEDLINE=21359325; PubMed=11466286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                          Matches 184; Conservative
                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clostridium
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DDI=10.1128/UB1.15.408.4-9632.7001;

ADD=10.1128/UB1.15.408.408.4-9632.7001;

Adibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Atusova R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,

Batusova R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,

Batusova R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,

Batusova R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,

Bally M.J., Bennett G.N., Koonin E.V., Smith D.R.;

Cenome sequence and comparative analysis of the solvent-producing

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RT "Genome sequence and comparative analysis of the solvent-producing

RT "Genome sequence and comparative analysis of the solvent-producing

RT Battle AR78403.1; -

DR REL, AR78403.1; -

DR REL, AR8051; H96551

RESEL, AR78403.1; -

DR RESEL, Profile Reservative Research Prospholistidine-sugar phospho. .; IER

GO; GO:0006891; F:sugar porter activity; IER.

GO; GO:0006810; P:transport; IER.

GO; GO:0006810; P:transport; IER.

DR RICEPRO; IPR001254; Peptidase Ell.

DR InterPro; IPR001254; Peptidase Ell.

DR Remi; PR00355; PTS Ells. 1.

DR Ptem; PR00355; PTS Ells. 1.

DR Ptem; PR00357; PTS Ells. 1.

DR Ptem; PR00354; PTS Ells. 1.

DR Ptem; PR00354; PTS Ells. 1.

DR Ptemp, PR00354; PTS Ells. 1.

DR Ptemp, PR00354; PTS Ells. 1.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      627 AA; 67596 MW; B835AB0238FCA436 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.1%; Score 759.5; DB 2; 36.7%; Pred. No. 9.2e-41; ive 80; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00371; PTS EIIA 1; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KAAGYEVTTPIVVSNYKKTGPVNT 443
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| KEKAVSPIVLTIVTNHEDMGFVNS 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 163; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome. SEQUENCE 627 AA;
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Q

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Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                             480 AA
                                                                                                                                                                                                       411 LCEFDIDAIKAAGYEVTTPIVVSN 434
                                                                                                                                                                                                                                           577 LVTFDIAAIKEAGYPVVTPIVVTN 600
                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X69800; CAA49461.1; -.
                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EC 2.7.1.69) (EII-Scr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus xylosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1288;
                                                                                                                                                                                                                                                                                                                                                           STAXY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LWQVLVMFGMHWGFVPIMMLNLTQGGDTWVPMLLPAVIAQGGAALAVFFLTKNVKLKGLA 352
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LSSSITTIFGITEPTVYGVTLPLKKPFIAACIGGGIGGAFVAMMHVKNFTFGLVSMLSLP 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . .; IEA.
                                                                                                                                                                                                                                                                         STRAIN-V583 / ATCC 700802,
MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
Paulsen I.T., Banerigi L., Myers G.S.A., Nelson K.E., Seshadri R.,
Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.
Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
                                                                                                                                                                Enterococcus faecalis (Streptococcus faecalis).
Bacteria, Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTK
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R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0008921; F:protein-N(FI)-phosphohistidine-sugar phosph. .;

R GO; GO:0009401; F:sugar porter activity; IEA.

R GO; GO:0009401; F:phosphoenolpyruvate-dependent sugar phospho. .;

R GO; GO:000810; F:transport; IEA.

R InterPro; IPR001295; Ptrans EIIE.

R InterPro; IPR001295; Ptrans EIIE.

R InterPro; IPR00127; PTS EIIA.

R InterPro; IPR00127; PTS EIIA.

R Pfam; PF00358; PTS EIIB; 1.

R Pfam; PF00358; PTS EIIB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Role of mobile DNA in the evolution of vancomycin-resistant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          626 AA; 66244 MW; 0E0BFB2C4220570B CRC64;
                                                         01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
PTS system, beta-glucoside-specific IIABC component.
OrderedLocusNames=EF2598;
                            626 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD001476; Ptrans EIIB; 1.
ProDom; PD002243; PTS EITA; 1.
TIGRFAMS; TIGR00830; PTSA; 1.
TIGRFAMS; TIGR01895; PTS-II-ABG-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00371; PTS_EIIA_1; UNKNOMN_1.
PROSITE; PS01035; PTS_EIIB_CYS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterococcus faecalis.";
Science 299.2071-2074 (2003).
EMBL; AE016555; AAO82308.1; --
HSSP; P08837; 1GGR.
                        PRELIMINARY;
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                                           Q831B4;
01-JUN-2003
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                        Q831B4
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TIGR;
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295 AEAE---APAEFS-NDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSP 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus xylosus.";

Mol. Gen. Genet. 241:33-41(1993).

-!- FUNCTION: This is a component of the phosphoenolpyruvate-dependent sugar phosphotransferase system (PTS), a major carbohydrate active transport system. The ILOD domains contain the sugar binding site and the transmembrane channel; the IIA domain contains the primary phosphorylation site (the donor is phospho-HPr); IIA transfers its phosphoryl group to the IIB domain which finally transfers it to the sugar.
                                                     461 TETDKWVAPVKTNQBDKILLASPLQGELLPLEKVQDPVFASGALGKGVAIEPTEGKLYAP
                                                                                                                                                                     351 VSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDBVKAGEL
                                                                                                                                                                                                                               BC component)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: Protein N-phosphohistidine + sugar = protein histidine + sugar phosphate.
histidine + Sugar phosphate.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
-!- SIMILARITY: Contains 1 PTS EIIB domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the sucrose-
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01-0CT-1996 (Rel. 34, Last sequence update)
05-0UL-2004 (Rel. 44, Last annotation update)
PTS system, sucrose specific IIBC component (SIIBC-Scr) (Sucrose-permase IIBC component)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR, S39998; S39978.

R InterPro; IPR001996; Ptrans_EIIB.

InterPro; IPR001956; Ptrans_EIIB.

R InterPro; IPR010972; PTS_II_BC_sucr.

Pfam; PF00367; PTS_EIIB; 1.

R Pfam; PF00378; PTS_EIIB; 1.

R ProDom; PD001476; PTS_EIIB; 1.

R TIGRFAMS; TIGR01995; PTS-III ABC-beta; 1.

R TIGRFAMS; TIGR01995; PTS-III -BC-sucr; 1.

R TIGRFAMS; TIGR01995; PTS-III -BC-sucr; 1.

R TIGRFAMS; TIGR01992; PTS-III -BC-sucr; 1.

R TIGRFAMS; TIGR01995; PTS-III -BC-sucr; 1.

R TIGRFAMS; TIGR01995; PTS-III -BC-sucr; 1.

R TIGRFAMS; TIGR01992; PTS-III -BC-sucr; 1.

R TIGRFAMS; TIGR01995; PTS III -BC-sucr; 1.

R SOUGHT; PS01035; PTS EIIB -BC-Si.

SUGAR transport; Transferase; Transmembrane.
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MEDLINE=94049666; PubMed=8232009;
Wagner B., Goetz F., Bruckner R.;
"Cloning and Characterization of the scrA gene encoding t
specific Enzyme II of the phosphotransferase system from
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Search completed: Od
Job time : 201 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of the alkaliphilic bacterium Bacillus of Complete genome sequence comparison with Bacillus subtilis.";

"Incleic Acids Res. 28:4317-4331(2000).

"Nucleic Acids Res. 28:4317-4331(2000).

"REL, APOULSOB, BAB04015.1;

"REL, APOULSOB, BAB04015.1;

"RESP, P20166; 1AX3.

"RESP, P20166; 1AX3.

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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2004 (TrEMBLrel. 26, Last annotation update)
PTS system, beta-glucoside-specific enzyme II, ABC component.
                                                                                                  (By similarity)
         BIIB.
EIIC.
Phosphocysteine (By similarity)
                                                                                                                                                                                              DB 1; Length 480;
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Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Mt
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 GFLGVVSIDAPD--MVMFLVCAVVTFFLAFGAAIAYGLYLVRRN 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus NCBI_TaxID=86665;
                                                                                                  Phosphohistidine (By simi AB4E1D9785D84E47 CRC64;
                                                                                                                                                                                              Query Match 29.7%; Score 701; DB 1; Best Local Similarity 51.4%; Pred. No. 4.1e-37; Matches 146; Conservative 49; Mismatches 81;
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InterPro; IPR011297; PTS EIIA.
InterPro; IPR011297; PTS EIIA.
InterPro; IPR011297; PTS EIIA.
Pfam, PF00358; PTS EIIA.
Pfam; PF00367; PTS EIIB; 1.
ProDom; PD001476; Ptrans EIIB; 1.
ProDom; PD001243; PTS EIIA; 1.
TIGREAMS; TIGR00830; PTRA, 1.
TIGREAMS; TIGR01995; PTS-II-ABC-beta; 1.
         26 EI
26 Ph
325 Ph
51326 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Q9KG19;
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                                                                                                                                                                                            236
                                                                                                                                                                                                                             RIKGTADFLITPVLTLLLTGFLTFIALGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLV 121
                                                                                                                                                       61
                                                                                                                                                                             122 YSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLAVFFLAKSBKLKGLA
                                                                                                                                                                                                                                                                                                                                                                                          GASGVSAVLGITEPALFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 SI---DAPDMVMFLVCAVVTFFIAFGAALAYGLYLVRRNGSIDPDATAAPVPAGTTKAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 EAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BDDKKEPSASEEIKSPLKGEVVPLTEVQDHVFSSGAMGKGVAVRPKEGRLVAPINGTVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 AFPSGHAFAVRIKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDID
                                                                                                                                                2 AMVFPŞLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHK
                                                                                                                                                                                                                                                      237 KIHEAVKNIVTELILLIVVIVPVTLILLGPIGUXLGNGIASVIQEIFTESPVLAGAIVAGI
                                                                                                               Gaps
                                                                                                               21;
                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   418 AIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAK 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                     6F0218011686ADD5 CRC64;
                                                                        Query Match
29.4%; Score 695.5; DB 2;
Best Local Similarity 32.8%; Pred. No. 1.2e-36;
Matches 152; Conservative 108; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    completed: October 29, 2004, 23:14:21
PROSITE; PS00371; PTS_EIIA_1; 1.
PROSITE; PS01035; PTS_EIIB_CYS; 1.
SEQUENCE 630 AA; 66978 WW; 6FC
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
               Copyright
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OM protein - protein search, using sw model

Run on:

October 29, 2004, 23:05:49 ; Search time 40 Seconds (without alignments) 1125.736 Million cell updates/sec

Title: Perfect score:

US-09-604-231-2 2363 1 MAMVFPSLVNGYDVAATMAA.....IEAGANLLNVAKKEAVPATP Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB : Maximum DB :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	phosphotransferse		firston pro system	ביים לכי	vstem. bet	sphotrans	PTS system, beta-d	system,	sphotrans	trehalose PTS svst	n.	System IIABC	sphotransferas	PTS SVStem. SUCTOS	PTS System, sucros	sphotrans	beta-glucoside per		ical pr		beta-glucoside-spe	PTS system, beta-q	thetical	phosphotransferase	hypothetical prote		4	PTS SVSTem trebal	sphotrans
SUMMARIES	S44257	B32243	H96951	839978	H83686	AB1167	AC1436	C83724	868599	C95220	AD1078	F95200	E98067	F82432	D90038	A99084	I40406	JQ0781	T47097	B42603	AC1421	D97073	D86807	AC1204	A97935	B95067	C69725	H83926	C25977
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Score	1058.5	953.5	759.5	701	695.5	695	674	673.5	673	673	667	664	660	629	629	658	657	646	645	640	628		588.5	580	'n	570.5	570	569.5	LO.
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beta-qlucoside-spe	hypothetical profe	phosphotransferase	PTS SVRTEM: SILVEDS	phosphotransferase	sac operon requiat	PTS SYSTEM trebalo	levanslicrase sunth	PTS System trebalo	nhosphotransferase	trehalose specific	nhosphotransferses	protein-Nai-aboenh	DTC ayram engine	hypothetical prote	PTS enzyme II, ABC
AB1423	C89813	862331	H83881	WOEBST	139868	AG1231	JU0293	AF1585	A39938	A98281	C65236	AI0449	A86122	A89781	B96970
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640	475	456	458	455	372	494	459	494	460	473	473	483	473	681	665
21.5	21.0	20.7	20.6	20.0	19.8	17.3	17.2	16.8	16.5	15.5	15.5	15.5	15.2	14.7	14.6
509	496	489	487	473	467	408	406	396.5	390	367	367	367	360	348.5	345
30	31	32	33	34	35	36	37	38	ω 6	40	41	42	43	44	45

ALIGNMENTS

C;Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransferase t C;Keywords: phosphotransferase F;488-640/Domain: phosphotransferase system glucose-specific enzyme II, factor III homold

5 Gaps 23; Query Match 44.8%; Score 1058.5; DB 2; Length 651; Best Local Similarity 46.7%; Pred. No. 1.3e-64; Matches 221; Conservative 78; Mismatches 151; Indels 23;

254 KHIKGAFDFTFTPMFAIVITGFLTFTIVGPVLRTVSDALTNGLVGLYNSTGWIGMGIFGL 313 g g à

177 KGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGF 236 ઠે

QQ

237 LGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAE 296 à 셤

297 AEAPAEFSNDSTIIQAPLIGEALALSSVSDAMFASGKLGSGVALVPIKGQLVSPVSGKIV 356 487 à qq

357 VAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDBVKAGELLCEFDI 416 à 원

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A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Recession: H96951
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-627 < KUR>
A; Residues: 1-627 < KUR>
A; Residues: 1-627 < KUR>
A; Residues: 1-627 < KUR>
A; Reperimental source: Clostridium acetobutylicum ATCC824
A; Reperimental source: Clostridium acetobutylicum ATCC824
C; Genetics:
A; Rene: CAC0423
C; Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransferase &
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Cipate: 13-dan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
Cipate: 13-dan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
Cipate: 13-dan-1997 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
Riwagner, E.; Goetz, F.; Brueckner, R.
Mol. Gen. Genet. 241, 33-41, 1993
A.Title: Cloning and characterization of the scrA gene encoding the sucrose-specific enz A.Reference number: 839976; MulD:94049686; PMID:8232209
A.Accession: 839978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 VSIDAPDMVMFLVCAVVTFFIARGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEA 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80; Mismatches 176;
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; Pred. No. 2.2e-40;
49; Mismatches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                             32.1%; Score 759.5; ilarity 36.7%; Pred. No. 3e-Conservative 80; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            443
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Best Local Similarity 51.4%;
Matches 146; Conservative 4
Bacteriol. 183, 4823-4838,
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Best Local Similarity
Matches 163; Conserv
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C;Species: Streptococcus mutans
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
T;Sato, Y:; Poy, F:; Jacobson, G.R.; Kuramitsu, H.K.
J. Bacteriol. 171, 263-271, 1989
A;Title: Characterization and sequence analysis of the scrA gene encoding enzyme II(scr)
A;Reference number: A32243; MUID:B9123027; PMID:253656
A;Accession: B3243
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Matches 205; Conservative
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A;Reference number: AB1077; MUID:21537279; PMID:11679669
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A;Cross-references: UNIPROT:Q8Y904; GB:NC_003210; PIDN:CAC98816.1; PID:g16410127; GSPDB:<A;Experimental source: strain EGD-e
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accessor, AC1436
F;Glasser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.
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185 ALVYPTMINLENEGAHITFLQIP------VVLMSYSFSVIPIILAVWFLSILBRFINS 236
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                              630
                   588 RITAAGYDVITPVLITNAKQFSNVQTTDKREVTSEDLLIHVIK
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EFDLEAIKADGYDITTPIVVTN
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Best Local Similarity 34.89
Matches 154; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTS system, beta-glucoside-specific enzyme II, ABC component BH0296 [imported] - Bacillu CiSpecies: Bacillus halodurans CiSpecies: Bacillus halodurans CiDate: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004 CiAccession: H8368  
R;Takami, H; Nakasone, K; Takaki, Y; Maeno, G; Sasaki, R; Masui, N; Fuji, F; Hira A; Takami, E; Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132  
A;Accession: H8368  
A;Status: preliminary A;Molacule type: DNA A;Residues: 1-630 <STO>
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C;Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransferase
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A;Experimental source: strain C-125
                                                                                                                                                            120 LVYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGAACLAVFFLAK-SE 174
MILVHPELMSAYDYPKALEAGKEIPHWNLFGLEINQVGYQGQVLPMLVATYILATIEKGL 253
                                                                                   314 LIYAPIVIIGMHHSFIAIETQLIADSSSTGGSFIFPIATMSNIAQGAALAAFFIIKENK 373
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29.4%; Score 695.5; DB 2;
Best Local Similarity 32.8%; Pred. No. 7e-40;
Matches 152; Conservative 108; Mismatches 182;
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          Science 294, 849-852, 2001
Abjuthors: Kreft, J.; Kunh, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Majauthors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Chlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Reference number: AB1077; MUD:21537279; PMID:11679669
A; Reference number: AB1077; MUD:21537279; PMID:11679669
A; Residual type: DNA
A; Residuals preliminary
A; Molecule type: DNA
A; Residuals: 1-633 < GLA>
A; Residuals: 1-633 < GLA>
A; Residuals: 1-633 < GLA>
A; Canetics: A; Canetics: Strain Clip11262
A; Experimental source: strain Clip11262
A; Genetics: A; Canetics: A; Canetics: A; Canetics: A; Canetics: A; Canetics: A; Canetics: A; Canetics: A; Canetics: A; Canetics: A; Canetics: A; Canetics: A; Canetics: A; Canetics: A; Canetics: A; Canetics: A; Canetics: A; Canetics: C; Superfamily: phosphotransferase
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                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                      30;
                                                                                                                                                                                                                                                                    Length 633;
                                                                                                                                                                                                                                                                tch 28.5%; Score 674; DB 2; Length 63 al Similarity 36.2%; Pred. No. 2.1e-38; Indels 161; Conservative 75; Mismatches 179; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  || ||||: |||||:||||:|
LLTEFDIEGIKAAGYDVTTPVVVTN 607
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RESULT 8
C83724
FYS system, beta-glucoside-specific enzyme II, ABC component bglP [imported] - Bacillus C; Species: Bacillus halodurans
C; Species: Bacillus halodurans
C; Date: 0.1-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C; Accession: C83724
R; Takami, H:) Nakasone, K:; Takaki, Y:, Maeno, G:; Sasaki, R:; Masui, N:; Fuji, F:; Hira Nucleic Acids Res. 28, 4317-431, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A83650; MUD:20512582; PMID:11058132
A; Accession: C83724
A; Ministric Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-636 c8TO>
A; CROSS-references: UNIPROT:Q9KF90; GB:AP001509; GB:BA000004; NID:gl0173176; PIDN:BAB043
A; Experimental source: strain C-125
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VYSPIVITGIHQSFPPIELELFNQGGSFIF-ATASMANIAQGAACLAVFFLAKSEKLKGL 179

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<u>:</u>

121

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phosphotransferase

Length 636;

DB 2;

Score 673.5;

28.5%;

Query Match

Genetics

A,Gene: bglP C,Superfamily: phosphotransferase system enzyme II sucrose-specific,

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- Streptococcus sobr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: scrA
S.Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransferase
C;Keywords: phosphotransferase; sugar transport system
F;480-632/Domain: phosphotransferase system glucose-specific enzyme II, factor III homol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphotransferase system enzyme II (EC 2.7.1.69), sucrose-specific - Streptococco phosphotransferase system enzyme II (EC 2.7.1.69), sucrose-specific - Streptococcus N,Alternate names: sucrose-specific enzyme II
C;Species: Streptococcus sobrinus
A;Variety: strain 6715
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C;Accession: S68599
R;Chen, Y.Y.M.; Lee, L.N.; LeBlanc, D.J.
Infect: Immun. 61, 2602-2610, 1993
A;Title: Sequence analysis of scrA and scrB from Streptococcus sobrinus 6715.
A;Reference number: S68599
A;Status: preliminary
A;Accession: S68599
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-632 cHE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAMVFPSLVNGYDVAATWAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIBKFLH
                                                                                                                                                                                                                                                108 DFGGPVGGLLFGLVYSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLA
                                                                                                                                                                                                                                                                                                                                                                                                                          227 KAVALGAAGFIGVVSI----DAPDMVMF-LVCAVVTFFIAFGAAIAYGLYLVRRNGSIDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   415 QGYIIGGLGIFGIPSFLHPADGMDAGFWGIVIAVVVAFV-LGFILTYLFGLKSGNASDBQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 DATAAPVPAGTTKAEAEAPAEFSNDSTLIQAPLTGEALALSSVSDAMFASGKLGSGVALV
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                                                                                                                                                                                         48 VSWILATIEKFLHKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLY
                                                                       - - GLDVAQAGYQGTVLPVLV
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28.5%; Score 673; DB 2; Length 63:
Best Local Similarity 36.4%; Pred. No. 2.4e-38;
Matches 168; Conservative 76; Mismatches 197; Indels
                             Indels
           Pred. No. 2.2e-38;
Hismatches 193;
                                  Mismatches
                                                                         AMVFPSLVNGYDVAATMAAGEMPMWSLF--
34.0%; F±-
                  Best Local Similarity 34.0
Matches 163; Conservative
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A;Molecule type: DNA
A;Residues: 1-634 <GLA>
A;Experimental source: strain EGD-e
C;Genetics:
A;Experimental source strain EGD-e
C;Genetics:
A;Gene: lmo0027
C;Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransferase s
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A, Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat A; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Ritle: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                      338 VAIVPTKGQLVSPVSGKIVVARPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNP 397
                                                                                                                                                                                                                                                                                                  241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AD1078
PTS system, beta-glucosides specific enzyme IIABC homolog lmo0027 [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD1078
                                                                                                                      EKFLHKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGG
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                                                                                                                                                                                                                                             LKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSN-
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Best Local Simil
Matches 156; (
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Ciscession: C95220
Rifettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid nson, T.; Hickey, E.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
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A;Modecule type: DNA
A;Rodides: 1-655 <KUR>
A;Cross-references: UMIPROT:097NW9; GB:AE005672; PIDN:AAK75956.1; PID:g14973388; GSPDB:
A;Experimental source: strain TIGR4
306 LQQVIVVTGVHHIFNFLETQLLAETKANPFNPLLSAATAGQVGAVLAVAVKTKSAKLKAL 365
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28.5%; Score 673; DB 2; Length 65:
Best Local Similarity 35.3%; Pred. No. 2.5e-38;
Matches 170; Conservative 87; Mismatches 173; Indels
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A; Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A; Reference number: A97872; MUID:21429245; PMID:11544234
A; Accession: B38067
A; Status: preliminary
A; Modecule type: DNA
A; Residues: 1.627 < KMR>
A; Residues: 1.627 < KMR>
A; Residues: Sorian Sorian Streptococcus Streptococcus Sorian Streptococcus Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Streptococcus Sorian Sorian Sorian Streptococcus Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian Sorian So
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27.9%; Score 660; DB 2; Length 62
Best Local Similarity 34.3%; Pred. No. 1.8e-37;
Matches 159; Conservative 92; Mismatches 187; Indels
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                                                                                                                                  RESULT 12
F95200
PTS system IIABC components [imported] - Streptococcus pneumoniae (strain TIGR4)
PTS system IIABC components [imported] - Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
R;Tettelin, H; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, anson, T.; Hickey, E.K.; Holt, I.B.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphotransferase
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A;Gene: SP1722
C;Superfamily: phosphotransferase system enzyme II sucrose-specific;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
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.larity 34.3%; Pred. No. 9.8e-38;
Conservative 92; Mismatches 187; Indels
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Matches 159; Conserv
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A; Residues: 1-627 < KUR>
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A;Cross_references: UNIPROT:Q9KLT8; GB:AE004395; GB:AE003853; NID:g9658068; PIDN:AAF9655
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
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A,Gene: VCA0653
A,Map position: 2
C,Superfamily: phosphotransferase system sucrose-specific enzyme II, factor
                                                                               358 AFPAALSAFLGITEPAIFGVNLKFRKPFFLSLIAGAIGGGLASILGLAGTGNGITIIPĞT
                                                                                                                                                                                                                                            VVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAE
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                    VYSPIVITGLHQSFPPIELELFNQGGSFIF-ATASMANIAQGAACLAVFFLAKSEKLKGL
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                                                                                                                                                                                                                                                                                                                                                                                                                               AIKAAGYEVTTPIVVSN---YKKTGPVNTYGLGEIEAGANLLNV 458
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Length 479;

DB 2;

Score 659;

27.9%;

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R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
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                                                                                                                  1 MAMVFPSLVNGYDVAATWAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAA 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAMVFPSLVNGYDVAATMAAGE-MPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                             4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Best Local Similarity 48.6%; Pred. No. 1.6e-37;
Matches 139; Conservative 53; Mismatches 82; Indels
                                                 87; Indels
Local Similarity 49.3%; pred. No. 1.6e-37;
les 133; Conservative 46; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 LGVVSIDAPDMVMFLVCAVVTFFIAFGAAI 266
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A;Molecule type: DNA
A;Residues: 1-480 <KUR>
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Search completed: October 29, 2004, 23:15:05 Job time : 42 secs

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October 29, 2004, 23:14:30 ; Search time 130 Seconds (without alignments) 1167.177 Million cell updates/sec
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| cgm2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
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3: /cgm2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 10. Appl	Segmence 6404. An	Sequence 60875. A	Segmence 375, Ann	Segmence 13467. A	Semience 367 App	Semience 73843 A	Semience 253 Ann	Semience 74439 A	Semience 70209 A	Semience 6961 pr	Semience 26 Appl	Sequence 43922, A	
SUMMARIES ID	US-10-450-055-10	US-09-738-626-6404	US-10-282-122A-60875	US-10-474-776-375	US-09-815-242-13467	US-10-474-776-367	US-10-282-122A-73843	US-10-474-776-253	US-10-282-122A-74439	US-10-282-122A-70209	US-09-738-626-6961	US-10-450-055-26	US-10-282-122A-43922	
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Sequence 5658, Ap Sequence 12270, A Sequence 51493, A Sequence 10809, A Sequence 56917, A Sequence 76917, A	equence 55853, equence 57628, quence 12272, genence 44138, equence 75030,	Sequence 75/36, A Sequence 73/368, A Sequence 75/40, A Sequence 59437, A Sequence 72912, A Sequence 73912, A Sequence 73006, A	71894 71894 13794, 45789, 5822, 12942, 71596,	Sequence 52557, A Sequence 280, App Sequence 330, App Sequence 1089, A Sequence 47256, A Sequence 57245, A Sequence 45636, A
US-09-815-242-56 US-09-815-242-12 US-10-282-122A- US-09-815-242-10 US-10-282-122A- US-10-282-122A-	Þ	$\begin{array}{c} 10.282 - 122A - 7 \\ 110 - 282 - 122A - 7 \\ 110 - 282 - 122A - 5 \\ 110 - 282 - 122A - 5 \\ 110 - 282 - 122A - 7 \\ 110 - 282 - 122A -$	US-10-282-122A US-09-815-242-1 US-10-282-122A US-09-815-242-5 US-09-815-242-1	6 US-10-476-287 6 US-10-476-280 0 US-09-741-669-330 0 US-09-815-242-10089 10-09-815-242-10089 10-10-282-122A-42726 10-282-122A-57245 10-282-122A-57245
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455.5 345.5 144.6 38.5 14.6 38.5 14.3 36.5 14.3 14.2 14.2	1.5 14.0 9.5 13.9 323 13.7 323 13.7 323 13.7 13.7 13.6	. 55 . 55 . 55 . 55 . 55 . 55 . 55 . 5		299 12.7 298.5 12.6 298.5 12.6 298.5 12.6 298.5 12.6 293.5 12.6
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ALIGNMENTS

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                                                                                                                                                                           SGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIK 420
                                                                                                                                                                                                                 2 AMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHK 61
494 AEFSNDSTIIQAPLITGEAIALSSVSDAMFASGKLGSGVAIVPIKGQLVSPVSGKIVVAFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                               AAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKKEAVPATP 468
                                                                                                                                                                                                                                                                                                        Length 617;
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34.8%; Pred. No. 3.2e-51;
live 82; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-09-36
PRIOR FILING DATE: 2000-09-36
PRIOR APPLICATION NUMBER: 60/23,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/25,578
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-22
PRIOR PELING DATE: 2001-02-09
PRIOR PELING DATE: 2001-02-09
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PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 60875, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 29.49
Best Local Similarity 34.89
Matches 154; Conservative
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Forsyth, R.
Xu, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carr, Grant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 SIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEAP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 MAMVFPSLVNGYDVAATWAAGEMPNWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH 253
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                                                                                                              241 SIDAPDWVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEAP 300
                                                                                                                                                              301 AEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFP 360
                                                                                                                                                                                               SCHAFAVRIKAEDGSNVDILMHIGFDIVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIK 420
               181 GASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVV 240
                                                                                                                                                                                                                                                                  SGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIK 420
                                                                  SIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAAAP 300
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100.0%; Pred. No. 1.7e-195;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE ALEBRANCE 177-120
CURRENT FILING DATE: 2000-12-18
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FLING DATE: 2000-04-07
PRIOR FLING DATE: 2000-08-03
NUMBER: OF SEQ ID NOS: 7059
SEQ ID NO 6404
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APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 6404, Application US/09738626; Publication No. US20020197605A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Corynebacterium glutamicum
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROS
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Matches 468; Conserv
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US-09-738-626-6404
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288 VPAGTIKAEAE----APAEFSNDSTI-----IQAPLIGEAIALSSVSDAMFASGKLGSG
                                            476 -TEGDTNLQAEFVAQEEAFVNHEPVELTSVEIISPLTGQVKELSQATDPIFASGVMGQG
                                                                                                                                                                                398 LKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSN---YKKTGPVNTYGLGELEAGAN
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27.9%; Score 660; DB 9; Length 62
Best Local Similarity 34.3%; Pred. No. 3.5e-48;
Matches 159; Conservative 92; Mismatches 187; Indels
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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryoes
FILE REPERENCE: ELITRA. 011.A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR PELING DATE: 2000-05-23

PRIOR PELING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

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Patent No. US20020061569A1
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: Zyskind, Judith W.
: Wall, Daniel
: Trawick, John D.
: Carr, Grant J.
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APPLICANT: Haselbeck, Robert
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TITLE OF INVENTION:
TITLE OF INVENTION: MOVEL STREPTOCOCCUS PREUMONIAE OPEN READING FRAMES ENCODING POLYFITLES OF INVENTION: ANTIGENS AND USES THEREOF
FILE REFERENCE: AM100649-PCT
CURRENT APPLICATION NUMBER: US/10/474,776
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 752
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 375
                                                                                                                                                                                                                                                                                                  GASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFL--- 237
                                                                                                                                                                                                                                                                                                                                       RLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWYGDVLAHGLQGLYDFGGPYGGLLFGLV 121
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                                                              238 -----GVVSIDAPDMVMFLVCAVVTFFIAFGAALAYGLYLVRRNGSIDPDATAAPVPAGT
                                                                                                                                                              YSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLA
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28.5%; Score 673; DB 16; Length 655;
Best Local Similarity 35.3%; Pred. No. 2.8e-49;
Matches 170; Conservative 87; Mismatches 173; Indels 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417 IFIGKGFVGFILGIAVAXILSAIGTYFFGYKDEMADGI----
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EFDLEAIKADGYDITTPIVVTN 591
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Publication No. US20040110181A1
GENERAL INFORMATION:
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LENGTH: 655
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87 AIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQGG 146
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PRIOR PILLING DATE: 2000-05-26
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PRIOR PILLING DATE: 2000-09-06
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PRIOR PILLING DATE: 2000-11-23
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PRIOR PILLING DATE: 2000-11-27
PRIOR PILLING DATE: 2001-11-27
PRIOR PILLING DATE: 2001-02-09
PRIOR PERIOR NUMBER: 60/257,931
PRIOR PILLING DATE: 2001-02-09
PRIOR PERIOR APPLICATION NUMBER: 60/267,636
PRIOR PILLING DATE: 2001-02-09
PRIOR PILLING DATE: 2001-02-09
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE REPERBNCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PRICA APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
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                                                    Sequence 73843, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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SEQ ID NO 73843
LENGTH: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Zyskind, Jud
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Best Local
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TITLE OF INVENTION: NOVEL STREPTOCOCCUS PNEUMONIAE OPEN READING FRAMES ENCODING POLYF
TITLE OF INVENTION: ANTIGENS AND USES THEREOF
FILE REPERBNCE: ANTIOG 49-PCT
CURRENT APPLICATION NUMBER: US/10/474,776
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 752
SOFTWARE: PATENTIN VETSION 3.1
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                                                        LGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLG-VVSIDAPDM
                                                                                                                                                        239 VVSIDAPDMVMFLVCAVVTFFIAFGAALAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAE
AGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT; ORGANISM: Streptococcus pneumoniae US-10-474-776-367
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Best Local Similarity 34.4
Matches 136; Conservative
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182 LIHPAFV-----AMVAEGKPL-TLFGAPVTPASYGSSVIPIIAMVYIMQXIEKWVNRL 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 SPIVITGLHQSFPPIELELFNQGGSFIFATASNA-NIAQGAACLAVFFLAKSEKLKGLAG 181
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                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 ASGVSAVL-GITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTWARE: PatentIn version 3.1 SEQ ID NO 74439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.9%; Score 564.5; DB 1
30.8%; Pred. No. 6.3e-40;
                                                                                                                                                                                                                                                                                                               FILE KEFEKENCE: ELLIKA, U34A

CURRENT PEPLICATION NUMBER: U5/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR PELICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-07

PRIOR FILING DATE: 2000-09-07

PRIOR FILING DATE: 2000-09-07

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-110-27

PRIOR PELICATION NUMBER: 60/257,931

PRIOR PILING DATE: 2000-112-27

PRIOR PELING DATE: 2000-112-27

PRIOR PELING DATE: 2000-112-27

PRIOR PELING DATE: 2000-12-27

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                                     Mang, Liangsu
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Publication No. US20040029129A1
GENERAL INFORMATION:
                                                                                                                                                                                                      Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Bublication No. US20040110181A1

APPLICANT: Wyeth
TITLE OF INVENTION:
TITLE OF INVENTION:
ANTIGENS AND USES THEREOF
FILE REFERENCE: AM10649-PCT
CURRENT FILING DATE: 2003-10-14

NUMBER OF SEQ ID NOS: 752

SOFTWARE: Patentin version 3.1

LENGTH: 612
                                                                                                424
          NDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 AIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQGG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFIFATASMA------NIAQGAACLAVFFLAKSEKLKGLAGASGVSAVL-GIT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --IFLAASIATPDVLILPAMLGSNLAQGAASWAVALKSKNNNTKQIAFAAGFSALLAGIT 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPAIFGVNLRLRWPFFIGIGTAAIGGALIALF----NIKAVALGAAGFLGV---VSIDAP 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -DWWMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEAPAEFS 304
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                                 462 NKKMIR-SPISGEIIPLSDVQDKTFSDKLIGDGVAIIPSEGKVYAPFDGKITNIFPTKHA
                                                                                      365 FAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGY
                                                                                                               27 SLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKRLKGTADFLITPVLTLLTGFLTFI
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Matches 143; Conservative
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ETVTPVIVTN 586
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ETVTPVIVTN 586
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31; Gaps

Length 620; Indels

DB 15;

297 AEAPAEFSNDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIV 356

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RESULT 9 US-10-282-122A-74439 ; Sequence 74439, Application US/10282122A

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289 PAGTIKAEAEAPAEFSNDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGVAIVPIKGQLV 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 GSFIFATASMANIAQGAACLAVFFLAKSEKLKGLAGAS--GVSAVL--GITEPAIFGVNL
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121 VYSPIVITGLHQSFPPIELELFNQ--GGSFIFATASMANIAQGAACLAVFFLAKSEKL--
                                                                                                177 -KGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAG
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29.8%; Pred. No. 1.5e-31;
tive 79; Mismatches 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE REPERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOUTWARE: Patentin ver. 3.0
SEQ ID NO 6961
                                                                                                                                                                                                      236 FLGV---VSIDAPDMVMFLVCAVVTFFI 260
                                                                                                                                                                                                                                                 330 VGGVPAFISIQKEFWPVYLIATAIALAV 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6961
                                                                                                                                                                                                                                                                                                                                                                         Sequence 6961, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 29.8%
Matches 141; Conservative
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IKEDA, MASATO
OZAKI, AKIO
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US-09-738-626-6961
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APPLICANT:
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,335
PRIOR PILING DATE: 2000-05-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
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               SQVKSGLSTKQT-LYAPMTGEMLFLSEVPDETFSSKLLGEGFAILPSEGEVYAPFDGEVI 520
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                                                                                              - See File Wrapper or PALM.
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Best Local Similarity 37.3%; Pred. No. 5.9e-34;
Matches 100; Conservative 63; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                                     ; sequence 70209, Application US/10282122A ; Publication No. US20040029129A1
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577 DFITSKGYSLISPVVVTN 594
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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                                                                                                                                                                                                                                                                                               RESULT 10
US-10-282-122A-70209
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Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
                                                                          Carr, Grant
Yamamoto, Robert
Forsyth, R.
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ORGANISM:
                                                         APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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       349 SPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDBVKAG 408
                          AIGPAMRWVGDVLAHGLOGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQ-G 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    278 LLGPFGIGVGNGISNLLEAINNFSPFILSIVIPLIYPFLVPLGLHWPLNAIMIQNINTLG 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 YDFIQGPMGAWNFACFGLVTGVFLLSIKERNKAMRQVSLGGMLAGLLGGISEPSLYGVLL 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIA 261
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                                                                        461
                                                                                   BLLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKK 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26, Application US/10450055
Publication No. US20040043953A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT BASF Aktiengesellschaft
TITLE OF INVENTION: No. US20040043953A1e1 genes of Corynebacterium
FILE REFERENCE: 936 2000
CURRENT APPLICATION NUMBER: US/10/450,055
CURRENT PILING DATE: 2003-06-10
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Vers. 2.0
LENGTH: 683
                                                                409 ELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                  47;
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                                                                                                                                                                                                                                                                                                                                                                                                                19.8%; Score 468.5; DB 1
llarity 29.8%; Pred. No. 1.5e-31,
Conservative 79; Mismatches 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 FGAAIAYGLYLVRRNGSID-----
                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-450-055-26
                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                           RESULT 12
US-10-450-055-26
                                                                                                                                                                                                                                                                                                                                                                                                                                          141;
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Best Local S
Matches 141
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Sequence 43922, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
APPLICANT: Wang, Liangsu APPLICANT: Zamudio, Carlos APPLICANT: Malone, Cheryl

US-10-282-122A-43922

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APPLICANT: Xu, H. TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 I--LAFPMALIW--PTIQSGLNAFSTGLLDSNTGVAVFLFGFIKRLLIPFGLHHIFHAPF
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Best Local Similarity 24.4%; Pred. No. 3.5e-21;
Matches 133; Conservative 67; Mismatches 192; Indels 153; Gaps

    See File Wrapper or PALM.

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FRIOR APPLICATION NUMBER: 60/191,078
FRIOR FILING DATE: 2000-02-21
FRIOR APPLICATION NUMBER: 60/201,078
FRIOR FILING DATE: 2000-05-23
FRIOR FILING DATE: 2000-05-23
FRIOR APPLICATION NUMBER: 60/207,727
FRIOR APPLICATION NUMBER: 60/207,727
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-06
FRIOR FILING DATE: 2000-05-06
FRIOR FILING DATE: 2000-09-09
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-11-23
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FRIOR 
                                                                                    FILE REFERENCE: ELITRA, 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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14.6%; Score 345.5; DB 9;
Best Local Similarity 24.2%; Pred. No. 6.4e-21;
Matches 132; Conservative 68; Mismatches 192;
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SOFTWARE: FastSEQ for Windows Version 4.0
228 AVALG---AAGFLGVVSIDA-PDMVMF---
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
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; ORGANISM: Staphylococcus aureus
US-09-815-242-12270
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                                                                                                                        369 TKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTT
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                                          Gaps
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APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
FILER REPERENCE: ELITRA.011A
FILER REPERENCE: ELITRA.011A
FILENCE RELING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5658, Application US/09815242 Patent No. US20020061569A1
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US-09-815-242-5658
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Zyskind, Judith W.
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Trawick, John D.
Carr, Grant J.
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Best Local Similarity 24.2'
Matches 132; Conservative
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650 PIIVT 654
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Search completed: October 29, 2004, 23:26:24 Job time: 133 secs

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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2004
          Copyright
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OM protein - protein search, using sw model

Run on:

October 29, 2004, 23:06:04; Search time 39 Seconds (without alignments) 795.816 Million cell updates/sec

Perfect score:

US-09-604-231-2 2363 1 MAWYFPSLVNGYDVAATMAA.....IEAGANLINVAKKEAVPATP Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

478139 segs, 66318000 residues

478139 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 seq] DB DB Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Issued Patents AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Sequence 3134, Ap		368.		3657			1057					3693				
US-09-543-681A-5773	US-09-134-001C-3134	US-09-107-532A-5798	US-09-634-238-368	US-09-543-681A-7659	US-09-134-000C-3657	US-09-489-039A-9162	US-09-252-991A-18115	US-09-489-039A-10571	US-09-107-532A-4365	US-09-107-532A-5592	US-09-583-110-4040	US-09-492-709A-352	US-09-134-000C-3693	US-09-583-110-5074	US-09-107-532A-5352	US-09-252-991A-19278	US-09-134-001C-4303
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269.5	197	266.5	260	256	248	244	230	223	181.5	159	157	151.5	144	141.5	139.5	137	136.5
28	, k	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 5822, Application US/09134000C
Sequence 5822, Application US/09134000C
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE REPERBANCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 5822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Enterococcus faecalis
US-09-134-000C-5822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: EDCE:
US-09-134-000C-5822
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29; Gaps Query Match
Best Local Similarity 39.3%; Pred. No. 2.4e-75;
Matches 184; Conservative 84; Mismatches 171; Indels 29 1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH

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61 KRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWYGDVLAHGLQGLYDFGGPVGGLLFGL 120 121 VYSPIVITGLHQSFPPIELELFNQ-----GGSFIFATASMANIAQGAACLAVFFLAKSE 174 234 GFLGVVSIDAPDMVMFLVCAVVTFFLAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTK 294 |||| :||:| : :|:| :::| : | | | : ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| : 95 KLKGLAGASGVSAVLGITEPALFGVNLRLRWPFFIGIGTAAIGGALLALFNIKAVALGAA 175 216 47 235 à 셤 ΩD ₹ g ð g g à

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GENERAL INFORMATION:
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                                                                                                                                                                                                    PARLERAL NO. 803703

GRERRAL NO. 803703

GRERRAL HOCKMATION:
APPLICANT: Lynn Doucette-Stamm et al.
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
FILE REFERENCE: PATHO0-07A
CURRENT APPLICATION NUMBER: US 60/526
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-06-12
PRIOR PRILING DATE: 1998-05-12
PRIOR PLILING DATE: 1998-05-12
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 3124
LENGTH: 627
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394 GIVQVVPETGHAYDLKS----NTGAEILIHVGIDTVSLNGKGFT--KKVGAKQKVKKGEV 447
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                                                  411 LCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLINV 458
                                                                      448 LGTFDSTVITNSGLDDTTMVIVTNSKDYSBVIPITKNIVTBGAALLTI 495
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20-09-107-532A-5288
; Sequence 5288, Application US/09107532A
; Patent No. 6583275
                                                                                                                                                                      Sequence 3124, Application US/09583110 Patent No. 6699703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Streptococcus pneumoniae
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                                                                                                                                                           US-09-583-110-3124
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US-09-583-110-3124
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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288 VPAGTTKAEAEAPAEFSNDSTIIQAPLJGEAIALSSVSDAMFASGKLGSGVAIVPTKGQL 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353 TKLRALGISSTVTSLFGITEPTVYGVTLPLKKPFIAACISGGIGGAIIGFSGVKAFSSSL 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 ---LGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAP 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LHKRLKGTADFLITPVLTLLIGFLTFIAIGPAMRWVGDVLAHGLQGL-
                                                                        NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
in NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...628
;
SEQUENCE DESCRIPTION: SEQ ID NO: 5288:
US-09-107-532A-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILLING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
PTLING DATE: July 2, 1997
                                                                                                                                                                                                                               ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                            COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                 STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 628 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 5288:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (781)893-8277
                                                                                                                                                                                      STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: July
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 33.5%
Matches 160; Conservative
                                                                                                                                                               CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                요
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BNTENCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ENTENCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 032796-032
CURRENT APPLICATION NUMBER: US 60/95/134,000C
CURRENT PILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4606
LENGTH: 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336 WOVCVIFGLHWGLVPLMINNMTVLGHDSMLPIILPAVIAOVGAVLGIFLATRDARORVLA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 RLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 YSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 GASGVSAVLGITEPALFGVNLRLRWPFFIGLGTAAIGGALIALFNIKAVALG-----AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 GFLGVVSIDAP-----DMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 VPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         498 -----GAVTVAPAS-AND---ILAPMSGSVIALEQVPDSTFASGLLGKGVALIPAVGQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 656;
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26.5%; Score 626.5; DB 4; Length
Best Local Similarity 33.5%; Pred. No. 2.6e-54;
Matches 158; Conservative 82; Mismatches 183; Indels
                                             Sequence 8212, Application US/09489039A
Patent No. 6610836
REPLICANT: GATY Breton et. al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4606, Application US/09134000C
Patent No. 6617156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Klebsiella pneumoniae
               JS-09-489-039A-8212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-489-039A-8212
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US-09-134-000C-4606
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| Patent No. 6699703
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
| TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
| TITLE OF INVENTION: Premomoniae for Diagnostics and Therapeutics
| TITLE OF INVENTION: PREMOMORER: US/09/583,110
| TITLE OF INVENTION: PAPHOLO-07A
| CURRENT FILING DATE: 2000-05-26
| PRIOR FILING DATE: 1998-06-30
| PRIOR PELLING DATE: 1998-06-30
| PRIOR PILING DATE: 1998-05-12
| PRIOR FILING DATE: 1998-05-12
| PRIOR FILING DATE: 1999-07-02
| WUMBER OF SEQ ID NOS: 5322
| SEQ ID NO 2958
                                                                348 VSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKOGDEVKA 407
                                                                                                             -----NKHANAGEPITSARHTLKSPLTGKVLPLSEVPDQVFSSGVMGKGIAIDPEVGEL 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 LHKRLKGTADFLITPVLTLLTGFLTFIALGPAMRWVGDVLAHGLQGLYDFG--GPVG-- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 WRKHIPEVISMIFVPFLSLIPALILAHTVLGP----IGWTIGQGLSSVVLAGLTGPVKWL 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 SEKLKG-LAGASGVSAVLGITEPALFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVAL 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIGGLPGILSIQPQYMLPPAGTMLVAIVVPMLLTP-----FFRKAGLFTKIEGDTN 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 AAPVPAGTTKAE--AEAPAEFSNDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGVAIVP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 343 TKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQG 402
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Larity 34.4%; Pred. No. 3.4e-57;
Conservative 91; Mismatches 177; Indels
                                                                                                                                                                                                                                                        ; ORGANISM: Streptococcus pneumoniae US-09-583-110-2958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
hes 165; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-583-110-2958
   466
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Matches
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1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 KRIKGTADFLITPVLTLLITGFLTFIAIGP----AMRWVGDVLAHGLQGLYDFGGPVGGL
                                                                                                                                                                                                                                                                                                                                                                              Query Match
24.7%; Score 583.5; DB 4; Length 583;
Best Local Similarity 29.1%; Pred. No. 4.8e-50;
Matches 139; Conservative 100; Mismatches 194; Indels 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
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CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
;
; LOCATION: (B) LOCATION 1...583
; SEQUENCE DESCRIPTION: SEQ ID NO: 681
US-09-107-532A-6811
                                                                                                                                                                                                                                         ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and
TITLE OF INVENTION: PREUMONIAE FOR DI
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REFERENCE/DOCKET NUMBER:
                     TELECOMMUNICATION: INFORMATION TELEPHONE: (781)893-5007
                                                                            INFORMATION FOR SEQ ID NO: 6811:
SEQUENCE CHARACTERRISTICS:
LENGTH: 583 amino acida
TYPE: amino acid
                                                         TELEFAX: (781)893-8277
                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                            ORIGINAL SOURCE
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US-09-583-110-2911
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                     229 VALGAAGFLGVVSI----DAPDMVMFLVCAVVTFFIAFGAAIAYGL-YLVRRNGSIDPDA 283
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                                                                                                                                                                                          WILATIEKFLHKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDF 109
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                                                                                                                                                                                                                                                                                                                                 GGPVGGLLFGLVYSPIVITGLHQSFPPIELFNQGGSFIFATASM-ANIAQGAACLAVF 168
                                                                                                                                                                                                                                                                                                                                                                   SPALYGLILGFFWQVLVIFGLHWSVVPLAIMQVIQEGSSQVLIGSFAASFAQTAVVLAMF 397
                                                                                                                                                                ---AQAGYQGTVLPVLVVS 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 TAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    344 KGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQCD
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                                                                                    Length 670;
                                                                                  25.8%; Score 609; DB 4; Length 670
30.9%; Pred. No. 1.6e-52;
.ive 85; Mismatches 200; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street
                                                                                                                                                                   2 AMVFPSLVNGYDVAA---TMAAGEMPMWSLFGLDV----
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APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: CD/ROM 1SO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
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STATE: Massachusetts
                             Enterococcus faecalis
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COMPUTER READABLE FORM
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                                                                                                                               Conservative
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                                                                                                            Best Local Similarity
Matches 146; Conserv
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US-09-107-532A-6811
                                                  US-09-134-000C-4606
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                                                                                           Query Match
                               ORGANISM:
            TYPE: PRT
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Nucleic Acid and Amino Acid Sequences Relating to Streptococcus Pneumoniae for Diagnostics and Therapeutics
                                                            116
117 LFGLVYSPIVITGLHQSFPPIELELFNQGGSF-IFATASMANIAQGAACLAVFFLAK-SE 174
                                                                                                                                                                          KIKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAA 234
                                                                                                                                                                                                                                                                  GFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNG---SIDP--DATAAPVP 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                        406 LQTANGATATPQSFEFVSA-----TGTAVATKETLFAVAAGTIKEITEVNDPVFSQKMM 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTH 394
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itent No. 0000000.
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
           238 RIVPEMVKVFMVPLLVILVSTPIALIAVGPVTSWFAQLIADGVILIQEHTGFIAIPLLVA 297
                                                                                                                                                                234 AGFLGV---VSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAFV-- 288
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517 MAIIPTTGKVIAPADGVVDITFSSGHAIGLILV----NNIEMLIHVGIDTVNLAGQHFTC 572
                                                                                                                                                                                                                                                                                             -----PAGTTK----AEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSG 337
                                                                  VYSPIVITGLHQSFPPIELELFNQGG--SFIFATASMANIAQGAACLAVFFLAKSEKLKG
                                                                                         464 EEENNKQAASTNKKPQIANSKLPVG-----LISPLQGKTVALSEVNDETFASGIMGPG
                                                                                                                                            LAGASGVSAVL-GITEPALFGVNLRLRWPFFIGIGTAAIGGALIALF----NIKAVALGA
                                                                                                                                                                                                                                                        414 PGLLSLPMWIS-DTDNQV---VNAIITLLIASVATFIATLII----GFDDP--TDDPIRD
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CVVKGQKVTKGDTLIBFDLDAIIAAGYDFTTMIIITN 609
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APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
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REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Enterococcus faecium
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Patent No. 6583275
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OPERATING SYSTEM: <Unknown>
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELEFAX: (781)893-8277
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SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
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GENERAL INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION: ULAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US 409/543,681A

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR APPLICATION NUMBER: US 60/128,706

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 7019
                                                                                                                                                                             12;
                                                                                                                                                                                                                              87 AIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQGG 146
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                                                                                                                                      Length 612;
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                                                                                                                                                                           Indels
                                                                                                                                      DB 4;
                                                                                                                             Query Match 24.2%; Score 572.5; DB 4
Best Local Similarity 33.3%; Pred. No. 6.7e-49;
Matches 143; Conservative 81; Mismatches 145
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Patent No. 6605709
                                                      TYPE: PRT
ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Proteus mirabilis
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Best Local Similarity 32.8 Matches 150; Conservative
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   SEQ ID NOS:
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                                                                                           US-09-583-110-2911
NUMBER OF SEQ
SEQ 1D NO 2911
LENGTH: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                     193
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48.2%; Pred. No. 2.9e-44;
iive 42; Mismatches 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4114
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CORRESPONDENCE ADDRESS:
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US-09-134-001C-4114
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                                                                                                                                                                                                                                                                                                                                                                                         | : | : | : | : | : | | SLHESIRNLITPFICIIVMVPIILLVVGFIADYASQLIAAGYLAVYNFSPVLSGAVIGGF 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFL--- 237
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                                                                                                                                                                                                                                                                                   ALVYPTIVSAYSDSITL-----RFLGMPVILARYTSTVIPAILAVWUSYIBPKIRK 260
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                                                                                                                                                           ; Score 562.5; DB 4;
; Pred. No. 7.2e-48;
84; Mismatches 169;
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22.7%; Score 537; DB 4;
Best Local Similarity 41.9%; Pred. No. 9.2e-46;
Matches 126; Conservative 41; Mismatches 108
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; Sequence 5482 Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
    TITLE OF INVENTION:
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                                           NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...631
SEQUENCE DESCRIPTION: SEQ ID NO: 3902:
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                                                                                                                                                                23.8%;
ilarity 30.3%;
Conservative 8
                                                                                                                                                                                            Local Similarity
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US-09-134-000C-5482
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                                                                                                                        US-09-107-532A-3902
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GENERAL OF GENERA APPLICANT: Lynn A Doucette-Stamm and David Bush TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS 'n 116 LEGLVYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGAACLAVFFLAK 172 173 -SEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVAL 231 374 GSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVS 433 - EGVELLIMHIGMDTVELDGKGFELSVKQGDSVKKGDLLVTFDIAAIKEAGYPVVTPIVVT 289 72 FFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAE---APAEFS-NDSTIIQAP 313 FILAEVLT-----FYLRFEDQPNPE-----TATEKTETDKWVAPVKTNQEDKIILASP 173 LIGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAED 373 73 IPGILYAPIVITGMHHIFIAVETTLIADATKTGGSFİFPIATMSNIAQGGAALAAFFIIK 57 KFLHKRLKGTADFLITPVLTLLITGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGL 15;

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Sequence 4715, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: EXTEROCOCCUS FABCALIS FOR DIAGNOSTICS AND THERAPEUTICS TILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR PAPLICATION NUMBER: US/09/134,000C
SPICE APPLICATION NUMBER: US/09/134,000C
NUMBER OF SEQ ID NOS: 6312
SOFTWARE: PATENT VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                       21.1%; Score 497.5; DB 4;
29.4%; Pred. No. 2e-41;
Live 87; Mismatches 183;
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                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4715
                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 133; Conservative
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US-09-489-039A-13018
                                            US-09-134-000C-4715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 ALF-NIKAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVR--RNGS 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279 IDPDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKIGSGV 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256 ATETATVNEVP-----EKVVPQTSABSVTILSSVADGTVVSLDKASDPVFAQKAMGEGY 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339 AIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPL 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                399 KKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKIGPVNTYGLGEIEAGANLLNV 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLAVFFLAKSEK--LKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 VLVVSWILATIEKFLHKRLKGTADFLITPVLTLLTGFLTFIAIGPAMRWVGDVLAHGLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.2%; Score 501.5; DB 4; Length 29.5%; Pred. No. 5.7e-42; tive 87; Mismatches 192; Indels
ADDRESSEE: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street
                                                                                                                                      COMPOTER: PC
COMPAGE: PC
COMPAGE: PC
CORRENT SASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-7um-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: July 2, 1997
ATTORNEY/AGENT INTERMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...427

SEQUENCE DESCRIPTION: SEQ ID NO: 5530:
US-09-107-532A-5530
                                                                                                                                                                                                                                                                                                                                                        NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Enterococcus faecium
                                                                                                                         MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 5530:
SEQUENCE CHARACTERISTICS:
LENGTH: 427 amino acids
                                   CITY: Waltham
STATE: Massachusetts
                                                                                       ZIP: 02354
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 29.5
Matches 124; Conservative
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Sequence 13018, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUWONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 GGLLFGLVYSPIVITGLHQSFPPIELELF-NQGGSFIFATASMANIAQGAACLAVFFLAK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 SEKLKGLAGASGVSAVLGITEPAIFGVNLRLRW---PFFIGIGTAAIGGALIALFNIKAV 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 ALGAA---GFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349 EVLISDKVIEBEBEREVFEMQHNTLDBQLFSPVTGYAMNLTAVNDPVFSSEMMGKGIAIMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343 TKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQG
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                                                                                                                                                                                                                                                                1 MAMVFPSLVNGYDVA-----ATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILA
                                                                                                                                           Gaps
                                                                                                                                           49;
Length 526;
                                                                                                                                           Indels
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
```

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213 LTHPALTNAWGVAAGFHTM------NFFGIEVAMIGYQGTVFPVLLAVWFMSNVEKRL 264
                                                                                                                  3 MVFPSLVNGYDVAA---TMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFL 59
                                                                     Query Match
20.7%; Score 489; DB 4; Length 483;
Best Local Similarity 38.5%; Pred. No. 1.3e-40;
Matches 104; Conservative 51; Mismatches 101; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                               237 LGVVSIDAPDMVMFLVCAVVTFFIAFGAAI 266
                                                                                                                                                                                                                                                                                                                            445 PGMAIVQASSLINYIIGMAIAFAVĀFALSI 474
; SEQ ID NO 13018
; LENGTH: 483
; TYPE: PRT
; CRGANISM: Klebsiella pneumoniae
US-09-489-039A-13018
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Search completed: October 29, 2004, 23:15:53 Job time : 41 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
               Copyright
```

OM protein - protein search, using sw model

Run on:

October 29, 2004, 22:57:48; Search time 156 Seconds (without alignments) 1076.188 Million cell updates/sec

US-09-604-231-2

Title: Perfect score:

2363 1 MAMVFPSLVNGYDVAATMAA.....IEAGANLLNVAKKEAVPATP Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2002273 Total number of hits satisfying chosen parameters:

2002273 segs, 358729299 residues

Searched:

Minimum DB Maximum DB

seq length: 0 seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* 23Sep04:* geneseqp1980s:* A Genesed

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

	Description	Aab66707 C.olutami		-	, μ	-			_	-	ţ.					t t					Abb49923 Listeria				Abba4803 Lactococc		ADD81450 Streptoco
SUMMERTES	ID	AAB66707	ABG80325	AAG92650	AAB69080	AAB66708	ADH87937	ABB47495	ABU32951	ABU02378	ABP81458	ADK46609	ABB49833	ABP25654	ADC95661	AAU37874	ABM72990	ADK46443	ABP25655	ABP27216	ABB49923	ABO61695	ADH86721	ABP27215	ABB54803	ARD81450	0010000
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	Query Match Length	468	468	199	199	362	496	617	617	655	655	627	634	919	628	627	287	655	674	620	617	929	670	639	636	381	i))
640	Query Match	100.0	100.0	100.0	98.7	77.1	35.2	29.4	29.4	28.5	28.5	28.3	28.2	28.1	28.0	27.9	27.9	27.7	27.4	26.7	26.6	26.5	25.8	25.0	24.9	24.8	1
	Score	2363	2363	2363	2332	1821	832.5	695	695	673	673	699	667	663.5	662	099	629	655	647.5	632	628	626.5	609	591.5	588.5	ന	
	Result No.	П	7	က	4	'n	9	7	∞	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	

Adc97184 E. faeciu			Adk46396 Streptoco						Adc94275 E. faeciu		Adh87597 Enterocon			Abb49939 Listeria				
ADC97184 ABB47649	ABP28755	ABU45919	ADK46396	ABU00950	ABP81336	ADF06734	ABP26854	ABU46515	ADC94275	ADN61668	ADH87597	ABU02198	ABP39269	ABB49939	ADC95903	ADH86830	ABU42285	ABM71603
7 13	Ŋ	9	ω	9	9	7	ß	9	7	œ	7	9	Ŋ	Ŋ	7	7	9	9
583	622	612	612	612	612	634	620	620	631	618	316	334	243	640	427	526	379	478
24.7	24.5	24.5	24.2	24.1	24.1	24.1	23.9	23.9	23.8	22.8	22.7	22.4	22.0	21.5	21.2	21.1	20.8	20.8
583.5	579	578.5	572.5	570.5	570.5	569	564.5	564.5	562.5	538	537	530	520.5	509	501.5	497.5	492	492
26	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Phosphoenolpyruvate; sugar phosphotransferase system; PTS. AAB66707 standard; protein; 468 AA (first entry) 09-APR-2001 AAB66707; RESULT 1 AAB66707

C.glutamicum phosphoenolpyruvate protein #1.

Corynebacterium glutamicum

WO200102583-A2.

11-JAN-2001

99US-0142691P. 99US-0150310P. 99DE-01042095. 99DE-01042097. 27-JUN-2000; 2000WO-IB000973 01-JUL-1999; 23-AUG-1999; 03-SEP-1999; 03-SEP-1999;

(BADI) BASF AG.

Zelder O, Haberhauer G; Schroeder H, Pompejus M, Kroeger B, WPI; 2001-080989/09. Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation.

Claim 4; Page 101-102; 144pp; English.

The present invention relates to Corynebacteium glutamicum phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation

Sequence 468 AA;

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                                                                                                                         KRIKGTADFLITPVLTLLITGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL 120
                                                                                                                                                    180
                                                                                                                                                                            180
                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metabolic pathway protein; MP; cell metabolism; amino acid; vitamin; cofactor; nucleotide; nucleoside; trehalose; fine chemical production; organic acid; non-proteinogenic amino acid; purine base; carbohydrate; pyrimidine base; lipid; unsaturated fatty acid; diol; polyketide; aromatic compound; food industry; animal feed; cosmetic industry;
                                                                                                                                                                                                                      VYSPIVITGLHQSFPPIELELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLA
                                                                                                                                                                      VYSPIVITGIAQSFPPIELEBENGGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLA
                                                                                                                                                                                                     GASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVV
                                                                                                                                                                                                                                                     SIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEAP
                                                                                                                                                                                                                                                                        AEFSNDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFP
                                                                                                                                                                                                                                                                                                                              AEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFP
                                                                                                                                                                                                                                                                                                                                                       SCHAFAVRIKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIK
                                                                            MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH
                                                   MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSW1LAT1EKFLH
                          Gaps
                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKKEAVPATP 468
  Length 468;
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                           Indels
100.0%; Score 2363; DB 4;
100.0%; Pred. No. 1.2e-226;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C. glutamicum metabolic pathway (MP) protein #5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG80325 standard; protein; 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmaceutical industry; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-DEC-2000; 2000WO-EP013143
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                            468; Conservative
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                 Local Similarity
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New metabolic pathway genes of Corynebacterium glutamicum for producing

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to the isolation of Corynebacterium glubulations metabolic pathway (MP) proteins, and the polynucleotide sequences encoding them. The MP proteins are enzymes involved in the metabolism of molecules important for the normal functioning of cells (e.g. amino acids, vitamins, cofactors, nucleotides and nucleosides, or trehalose). The polynucleotide sequences encoding the MP proteins are useful for producing fine chemicals, particularly organic acids, non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, aromatic compounds, vitamins, cofactors, polyketides and enzymes. The fine chemicals are useful in the food, animal feed, cosmetic or pharmaceutical industries. ABG880321-ABG80343 represent the C. glutamicum MP proteins of the invention
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            cofactors or enzymes used in food, feed, cosmetics or pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid synthesis; vitamin; saccharide;
(un) saturated fatty acids, vitamins,
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                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                               100.0%; Score 2363; DB 5;
100.0%; Pred. No. 1.2e-226;
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                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                           Claim 18; Page 111-113; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ā
                                                                                                                                                                                                                                                                                                                                                               0;
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   e.g. lipids,
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                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                        Sequence 468 AA;
   chemicals,
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                                    industries.
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AAG92650
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Ochiai K,

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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the Buropean Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VYSPIVITGLHQSFPPIELELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIK 613
                                                                                                                                                                                                                                                                                                                                                                          mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAMVFPSLVNGYDVAATWAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH
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                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; SEQ ID NO 6404; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                             H, Ando S, Hayashi M,
Ikeda M, Ozaki A;
                                                                                                                          16-DEC-1999; 99JP-00377484.
07-APR-2000; 2000JP-00159162.
03-AUG-2000; 2000JP-00280988.
                                                                                         18-DEC-2000; 2000EP-00127688
                                                                                                                                                                                                    (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                           Mizoguchi H
Senoh A, I
                                                                                                                                                                                                                                                                                                  WPI; 2001-376931/40.
                                                                                                                                                                                                                                                                                                                   N-PSDB; AAH67869.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 661 AA;
                   EP1108790-A2
                                                                                                                                                                                                                                           Nakagawa S,
Tateishi N,
                                                      20-JUN-2001
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The present sequence represents the Brevibacterium lactofermentum sucrose PTS (phosphoenolpyruvate:carbohydrate phosphotransferase system or phosphoenolpyruvate-sugar transport system) enzyme II, which has sucrosebinding activity. A coryneform bacteria produced with the sucrose PTS enzyme II gene can have more efficient sugar uptake, and improved aminodial and mucleic acid productivity. The sucrose PTS gene and it's disrupted gene, such as one without the sucrose PTS gene and it's to produce new breeds of coryneform bacterial strains to uptake sugar more efficiently e.g. glucose only or and sucrose, and can have improved amino-acid and nucleic acid productivity. (Updated on 11-SEP-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VYSPIVITGLHQSFPPIELELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLA 180
                                                                                                                                                                                                          Brevibacterium lactofermentum sucrose PTS enzyme II protein SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene encoding sucrose phosphoenolpyruvate-sugar transport system enzyme II obtained by cassette ligation-mediated amplification of downstream domain of coryneform bacterium sucrase gene, with sucrose-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 MAMVFPTLVNGYDVAATMTAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIBKFLH
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                                                                                                                                                                                                                                          Brevibacterium lactofermentum; sucrose PTS enzyme II; sucrase; phosphoenolpyruvate:carbohydrate phosphotransferase system; glucose; coryneform bacterium; phosphoenolpyruvate-sugar transport system.
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                       661
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Pred. No. 2.6e-223;
4; Mismatches 3; Indels (
Kurahashi O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 29-32; 45pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakamatsu T,
                                                                                                    ¥.
                                                                                               AAB69080 standard; protein; 661
                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000; 2000WO-JP004348.
                                                                                                                                                                                                                                                                                                                                                                                                                                        99JP-00189512
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98.5%;
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                                                                                                                                                                (revised)
(first entry)
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Matches 461; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sugimoto M,
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                                                                                                                                                             11-SEP-2003
20-APR-2001
                                                                                                                               AAB69080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Izui M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254
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                                                                 RESULT 4
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LVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVK 406
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                                                                                                        KAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFLAFGAALAYGLYLVRRNGSIDPDATAA
                                                                                                                                                             PVPAGTTKAEBAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQ
                                                                                                                                                                              VFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNI
                                                                                                                            YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQGGSFIFATASMANIAQGAACLA
                                                                              VFFLAKSEKLKGLAGASGVSAVLGTTEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNI
     YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQGGSFIFATASMANIAQGAACLA
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                                                                                                                                                                                                                                                                                                                        TP 468
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                                                   300
                                                                                                                           AEFSNDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGVAIVPIKGQLVSPVSGKIVVAFP 553
                                                                                                                                                       SCHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIK 420
                                                                                                                                                                              SGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIK 613
                       433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers
                                                                                                    AEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFP
              SIDAPDMVMFLVCAVVTFVIARGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEAP
GASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVV
                                                   SIDAPDWVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEAP
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                                                                                                                                                                                                        AAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLMVAKKEAVPATP 468
                                                                                                                                                                                                                         Haberhauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention relates to Corynebacteium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                        Phosphoenolpyruvate; sugar phosphotransferase system; PTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                C.glutamicum phosphoenolpyruvate protein #2
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                                                                                                                                                                                                                                                                                                    AAB66708 standard; protein; 362
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99US-0150310P.
99DE-01042095.
99DE-01042097.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium glutamicum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transformation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 362 AA;
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03-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                       09-APR-2001
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The invention relates to Enterococcus faecalis polynucleotides and polypeptides. The invention also relates to a recombinant expression vector comprising a polynucleotide operably linked to a transcription regulatory element, a cell comprising a recombinant vector, a method for producing an E. faecalis polypeptide, an isolated nucleic acid comprising a sequence not given in the specification, a recombinant vector
                                                                                                                                                                                                                                                                                                                                                                                      an Enterococcus fecalis
for diagnosing or
                                                                                              Enterococcus faecalis infection; transcription regulatory element; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid comprising a sequence encoding polypeptide, useful for preparing a composition treating B. fecalis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                            ID NO 5822; 193pp; English.
                                                                             Enterococcus faecalis polypeptide #2417.
Ā
ADH87937 standard; protein; 496
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                                                                                                                                                                                                                                                                                   DOUCETTE-STAMM L A.
                                                   (first entry)
                                                                                                                                                                                                                                                                                                                          Bush
                                                                                                                                               Enterococcus faecalis.
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N-PSDB; ADH84532.
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77.1%; Score 1821; DB 4; 1 ilarity 100.0%; Pred. No. 1.1e-172; Conservative 0; Mismatches 0;

Query Match Best Local Similarity Matches 362; Conserv

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comprising the nucleic acid and a cell comprising the recombinant vector. The polynucleotides can be used to detect the presence of B. faecalis in a sample. The sequences are useful for preparing a composition for diagnosing or treating Entercoccus faecalis infection. This sequence represents an B. faecalis polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 INTNQIANADEPTIVETIVSPLAGEITTLGSVNDPVFSSESIGKGIAIKPNGNTIYSPVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LCEFDIDAIKAAGYEVITPIVVSNYKKTGPVNTYGLGEIEAGANLLNV 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                             35.2%; Score 832.5; DB 7; 39.3%; Pred. No. 9e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84; Mismatches 171;
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                                                                                                                                                                                                                                                                                  Sequence 496 AA
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ftp.wipo.int/pub/published_pct_sequences

The present invention relates to the genome sequence of Listeria

CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of

it are useful for selecting probes and primers for detecting genes in L.

CC monocytogenes and related organisms, and for studying genetic

CC motocytogenes and related organisms, and for studying genetic

CC polymorphisms and other genomes. The present sequence is a protein

CC polymorphisms and other genome sequence are useful for raising specific

CC antibodies, identification of L. monocytogenes and related organisms, and

CC antibodies, identification of L. monocytogenes and related organisms, and

CC antibodies, identification of L. monocytogenes and related organisms, and

CC sequence and proteins encoded by it are also useful for

CC sequence and proteins encoded by it are useful in pharmaceutical and

CC sequence and proteins encoded by it are useful in pharmaceutical and

CC sequence and proteins encoded by it are useful in pharmaceutical and

CV accines compositions for the treatment or prevention of infections by L.

CC monocytogenes and related organisms. Note: The sequence date for this

CC patent did not form a part of the printed specification, but was obtained

CC in electronic format directly from NIPO at

CC in electronic format directly from NIPO at

omic sequence for Listeria monocytogenes, useful e.g. for treatment prevention of Listeria and related bacterial infections, and related

Claim 6; SEQ ID NO 200; 192pp; French.

polypeptides.

Genomic

Garrido-Garcia P, Tierrez-Martinez A, Amend A; nn E, Hain T, Berche P, Charbit A, Durant L; ro F, Garcia Del Portillo F, Gomez-Lopez N; os B, Wehland J, Kaerst U, Entian K, Hauf J;

Dominguez-Bernal G, Garri Chakraborty T, Domann E, Perez-Diaz J, Baquero F, Maduenio E, De Pablos B,

WPI; 2002-010914/01. Voss H;

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                                                                                                                                                                                                                                                                                                                                                                       62 RLKGTADFLITPVLTLLLIGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLV
                                                                                                                                                                                                                                                                                                                                                                                                           122 YSPIVITGLHOSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFL---
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                                                                                                                                                                                                                                                                                                                            Length 617;
                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                        29.4%; Score 695; DB 5; L. 34.8%; Pred. No. 6.7e-60; live 82; Mismatches 162;
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EFDLEAIKADGYDITTPIVVTN
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 34.88
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                      Sequence 617 AA;
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RESULT

Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P; Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;

11-APR-2001; 2001WO-FR001118. 11-APR-2000; 2000FR-00004629

18-OCT-2001

(INSP) INST PASTEUR

Length 617;

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the following tenates to an instance actual complements of the delay any must invention tenates to an instance actual complements of the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the mucleic acid encoding a polypeptide whose expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense confished acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular or proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway or the gene product or that has an activity against a biological pathway or proliferation; (7) identifying a compound that influences the activity of identifying a gene required for cellular proliferation or the biological pathway or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound; activity; (11) a culture comprising strains in which the gene compound that inhibits are sent of the strains is present in a culture or collection of an organism of the strains is present in a culture or collection of contound that inhibits are useful for proliferation of an organism. The antisense mucleic acids are useful for an organism or screening for homologous nucleic acids required for an allowary proverses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              drug discovery programs, or for screening homologous mucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               one of
                                                                                                                                                                    Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zyskind JW;
Xu HH;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohlsen KL,
Forsyth RA,
                                                                                                                                  encoded by Prokaryotic essential gene #18478.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 25; SEQ ID NO 60875; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
                  ABU32951 standard; protein; 617 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                   : 2001US-00815242.
: 2001US-00948993.
: 2001US-0342923P.
: 2002US-00072851.
: 2002US-0362699P.
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                                                                                               entry)
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Trawick JD,
                                                                                               (first
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N-PSDB; ACA36821.
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25-OCT-2001;
08-FEB-2002;
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                                                                                                 19-JUN-2003
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                                                                                                                     RIKGTADFLITTPVLTLLLTGFLTFIALGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antiinflammatory; antibacterial; immunostimulant; auditory; respiratory; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media
                                                                                                                                                        122 YSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLA
                                                                                                                                                                                                                                                                                                                                 ----GVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGT
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                                                  2 AMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHK
                                                                                                                                                                                                              GASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFL---
                           Gaps
                           44;
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                                                                                                                                                                                                                                                                                417 IFIGKGFVGFILGIAVAYILSAIGTYFFGYKDEMADGI----
                            82; Mismatches 162;
 29.4%; Score 695; DB 6; 34.8%; Pred. No. 6.7e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae; type 4 strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU02378 standard; protein; 655 AA.
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EFDLEAIKADGYDITTPIVVTN
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(first entry)
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(GENO-) INST GENOMIC RES.
Query Match
Best Local Similarity 34.8'
Matches 154; Conservative
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11-FEB-2003
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us-09-604-231-2.rag

Claim 1; SEQ ID NO 3912; 56pp; English.

Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a sequence not defined in the specification, for amplifying a target requence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target sequence of the target sequence, and where the parts of the primers having substantially complementary to the complement of the target sequence of the target sequence of the target sequence of substantially complementary to the complement of substantially complementary to the complement of the target sequence of and the second primer is substantially complementary to the complement of substantial complementarity define the termin of the target sequence of substantial complementary to define the termin of the protein substantial assay comprising contacting a test compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more genes conding the proteins has been rendered inactive. The proteins, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus cut reating or preventing a disease or infection due to streptococcus media or ear infection. They are also useful in developing vaccines, diagnostics and antibiotics. The methods are useful for identifying immunodominant proteins. The present sequence is one of the 2469 proteins were specification, but was obtained in electronic format directly from NIPO at the properties of field) fragment, The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fraggexpressed from 2469 of 2489 identified DNA coding regions from the

Sequence 655 AA;

52; Length 655; 28.5%; Score 673; DB 6; Length 65 35.3%; Pred. No. 1.1e-57; ive 87; Mismatches 173; Indels al Similarity 35.3 Query Match Best Local S Matches

195 ICLVSPQLLNAYAVASTPAADIAANWVWNFGYFTVNRIGYQAQVIPALLAGLSLSYLBIF 254 LHKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFG--GPVG-- 114 1 MAMVFPSIVNGYDVAATMAAGEMP--MWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKF Gaps à g 8

255 WHKHIPEVISMIEVPFLSLIFALILAHTVLGP----IGWTIGQGLSSVVLAGLTGPVKML 310 -GLLFGLVYSPIVITGLHQSFPPIELELF-NQGGSFIFATASMANIAQGAACLAVFFLAK 172

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-SEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVAL 173

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288 VPAGTTKAEAE----APAEFSNDSTI-----IQAPLIGEAIALSSVSDAMFASGKLGSG GIGGLPGILSIQPQYMLPFAGTMLVAIVVPMLTF------FFRKAGLFTK----431

338 VAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNP 397

LKKQGDBVKAGELLCEFDIDAIKAAGYEVTTPIVVSN---YKKTGPVNTYGLGEIEAGAN 454 GAAGFLGVVSIDAPDMVMF----LVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAP -TEGDTNLQAEPVAQEEARFVNHEPVELTSVEIISPLTGQVKELSQATDPIFASGVMGQG 398 232

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a Streptococcus pneumoniae genomic sequence, a fragment or degenerate variant of the polynucleotide or a nucleic acid sequence 95% identical to one of the polynucleotides. The S. pneumoniae polynucleotides and encoded polypeptides (ABPR1299-ABPR1674) are useful for treating or preventing S. pneumoniae infections or non-systemic diseases, e.g. othis media, which are induced or exacerbated by S. pneumoniae. These are also useful for pneumoniae in a biological sample or diagnosing S. pneumoniae in a subject. The polynucleotides have antibacterial activity and are useful in gene therapy The invention relates to isolated polynucleotides (ABZ72147-ABZ42522) of New Streptococcus pneumoniae polynucleotides, useful for treating or preventing S. pneumoniae infections, or non-systemic diseases, e.g. otitis media, which are induced or exacerbated by S. pneumoniae. Streptococcus pneumoniae; infection; otitis media; antibacterial; diagnosis; gene therapy. DP; Russell Streptococcus pneumoniae polypeptide SEQ ID NO 375. Chakravarti DN, Claim 42; Page 617-620; 1091pp; English. AA. Green BA, ABP81458 standard; protein; 655 12-APR-2002; 2002WO-US011524 16-APR-2001; 2001US-0283948P-18-APR-2001; 2001US-0284443P (AMCY) AMERICAN CYANAMID CO (first entry) Streptococcus pneumoniae. Masi AW, WPI; 2003-093010/08. N-PSDB; ABZ42306. 455 LL 456 |: 649 LM 650 WO200283855-A2 Zagursky RJ, 04-MAR-2003 24-OCT-2002. Wooters JL; ABP81458; RESULT 10 ABP81458 g ð

1 MAMVFPSLVNGYDVAATMAAGEMP--MWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKF 52; Gaps Length 655; 28.5%; Score 673; DB 6; Length 65: 35.3%; Pred. No. 1.1e-57; ive 87; Mismatches 173; Indels Query Match
Best Local Similarity 35.3%
Matches 170; Conservative à

Sequence 655 AA;

16;

LHKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWYGDVLAHGLQGLYDFG--GPVG---GLLFGLVYSPIVITGLHQSFPPIELELF-NQGGSFIFATASMANIAQGAACLAVFFLAK 59

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173 -SEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVAL 231 Length 627;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                LKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSN---YKKTGPVNTYGLGBIBAGAN 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid molecules and polypeptides useful for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, e.g. Streptococcus pneumoniae infection, and in drug
                                  430
                                                                                                                                                                                                                                                                                                                                    |: :: :| | ||:|||:||||: :|| |: || ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: 
                                                                                                                                                                                                                              - TEGDTNLQAEFVAQEEAEFVNHEPVELTSVEIISPLTGQVKELSQATDPIFASGVMGQG
                                                                                                                                                                                                                                                                                                        VAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNP
                                                                                  GAAGFLGVVSIDAPDMVMF----LVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAP
                                                                                                                                                                                              VPAGTTKARAE----APAEFSNDSTI-----IQAPLIGEAIALSSVSDAMFASGKLGSG
                                                                                                                                        ---FFRKAGLFTK----
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                                                                                                                                        431 GIGGLPGILSIQPQYMLPFAGTMLVAIVVPMLLTF---
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98US-0085131P.
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segdata.uspto.gov/sequence.html

Sequence 627 AA

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417
                                                                                                                                                                                                                                                                        239 VVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAE 298
                                                                                                                                                                                                                                                                                                                             -APARFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVV 357
                                                                                                                                                                                                                                                                                                                                                                                                               584
                        10;
                                                                                                                                                                                                                   238
                                                                                                                                                                                                                                    120
                                                                                                                          179
                                                                                                                                                                            Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P, Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P, Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Bonad JA; Dominquez-Bennal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Dominn E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                   09
                                                                                                                                                                                                                                                                                                                                                                                   358 AFPSGHAFAVRIKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDID
                                                                                                                                                                                                                                                                                                                                                                                                   KRLKGTADFLITPVLTLLLTGFLTFIALGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL
                                                  1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH
                                                                          182 MMLVSGSLPNAWAVA---QGGEVTAMNFFGF-IPVVGLQGSVLPAFIIGVVGAKFEKAVR
                                                                                                                                                            VYSPIVITGLHQSFPPIELELFNQGGSFIF-ATASMANIAQGAACLAVFFLAKSEKLKGL
                                                                                                                                                                                                                 AGASGVSAVLGITEPAIFGVNIRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLG-
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
                        26;
                                                                                                                                                                                                                                                                                                                                                                                                                                          418 AIKAAGYEVTTPIVVSN----YKKTGPVNTYGLGEIEAGANLLNV 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                         92; Mismatches 186;
Score 669; DB 8;
Pred. No. 2.7e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vitamin B12; bacterial infection; disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB49833 standard; protein; 634
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  28.3%;
34.5%;
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                              Conservative
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               Similarity
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    Query Match
Best Local Simil
Matches 160; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
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The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genets in L. colymorphisms and other genomes. The present sequence is a protein concoded by the genome sequence of the present invention. Proteins carpothesis and characteristication of L. monocytogenes and related organisms, and corp. The genome sequence are specially biosynthesis of vitamin of L. biosynthesis and biodegradation, especially biosynthesis of vitamin compounds that regulate gene expression and cell replication concerned and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication concerned and proteins encoded by it are useful in pharmaceutical and concorned sompositions for the treatment or prevention of infections by L. monocytogenes and related organisms. Note: The sequence data for this concorned form part of the printed specification, but was obtained for the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the con
                                              Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                             Claim 6; SEQ ID NO 2538; 192pp; French.
                                                                                                                                            polypeptides.
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Sequence 634 AA;

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                                                                                                                                                                                                  LLFGLVYSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLAVFFLAKSE 174
                                                                                                                                                                                                                                LILGGFWQVFVIFGLHWGLVPVAINNLTVLGHDPILAMTFGASFAQIGAVLAVFFKSRNK 361
                                                                                                                                                                                                                                                               KLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAA 234
                                                                                                                                                                                                                                                                                  GFLGVVSIDAP-----DMVMFLVCAVVTFFIAFGAALAYGL-----YLVRRNGSIDPDA 283
                                                                                                                                                                                                                                                                                                                                                          GIRGLPNFFREGSGISGEFWWVIAIVISFILGFILTYVVGFKDPADVVVEQSNIVE--- 478
                                                                                                                                                                                                                                                                                                                                                                                                                 -----GBTLIERET------IPAPVVGEIVTLADVKDEAFSSGALGKGVAIIPT 521
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                                                                                                                                                                   242 EKGFKKIIPDVIKTFVVPFCTLLIVVPITFİVİGPIATWAĞQLLGAĞTIWVYNLSPIIAĞ
                                                                      2 AMVFPSL--VNGYDVAATWAAG---EMPMWSLF-GLDVAQAGYQGTVLPVLVVSWILATI
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                           284 TAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPT
                                              42;
             Length 634;
                                             172; Indels
      28.2%; Score 667; DB 5; 34.6%; Pred. No. 4.3e-57; tive 81; Mismatches 172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                578 VIEKGQLLTEFDIEGIKAAGYDVTTPVVVTN 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVKAGELLCEFDIDAIKAAGYEVTTPIVVSN 434
                                         Conservative
Query Match
Best Local Similarity
Matches 156; Conserva
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ABP25654 standard; protein; 676 AA

RESULT 13

(first entry)

02-JUL-2002 ABP25654;

ABP25654 ID ABP2 XX AC ABP2 XX DT 02-J

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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus progenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detect Streptococcus in such as a vaccine or diagnostic composition. The disease caused by used as a vaccine or diagnostic composition. The disease caused by streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity encoding the process of the prography of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the 
                                               Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 FLAK-SEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIK 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.1%; Score 663.5; DB 5; Length 676; 35.3%; Pred. No. 1.1e-56; ive 82; Mismatches 195; Indels 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Masignani V, Margarit Y RosI, Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 3202-3203; 4525pp; English.
  Streptococcus polypeptide SEQ ID NO 484
                                                                                                                                                                                                                                                                                                                                                                        27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
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                                                                                                                                                                Streptococcus agalactiae.
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(GENO-) INST GENOMIC RES
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABN66285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 676 AA;
                                                                                                                                                                                                                   WO200234771-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Telford J,
Tettelin H;
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SXXCCCCCCCCCCCXXXHHLXXHHXXHHXXHKXHXXHXXHXXHXXHXXHXX
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Sequence 628 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid derived from CC Exterococcus faecium encoding an Enterococcus faecium polypeptide having C Exterococcus faecium encoding an Enterococcus faecium polypeptide having one of 10 fully defined sequences given in the (or comprising 40 sequential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridising to it). Also included are a recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The nucleic acids are chosen from 3654 disclosed sequences encoding 3654 disclosed proteins. The nucleic acids is useful for diagnosing pathological conditions cresulting from E. faecium bacterial infection (e.g. urinary tract infection, bacteraemia, endocarditis, wounds and abditions confection) and for screening drugs such as agonists and attagonists. The nucleic acid is useful for recombinant production of Candida albicans derived peptides or antisense polypeptides. Pharmaceutical compositions conditions the nucleic acid are useful for preventing or treating Enterococcus faecium infections. The present sequence represents one if the disclosed E. faecium proteins.
                                                                                                343
                                                                                                                                                                                             403
                                                                                                                                                                                                                                         617
                                                                                                                                    ---VIASTTETKSAKEKAVVSGTKLSVVSPLSGLAKPLDQASDPVFSQGIMGKGVVIDPS 561
                                                 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid derived from Enterococcus faecium encoding an Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial infection.
                                                                                                                                                                                                                                                                                   EVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGL-GEIEAGANLLNVAKK 461
                                                                                                                                                                                                                                                                                                                 AVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAY---GLYLVRRNGSIDPDAT
                                         285 AAPVPAGTTKAE-AEAPAEFSNDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGVAIVPT
                                                                                                                                                                                                                           KGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaccine; urinary tract infection; bacteraemia; endocarditis; wound; abdominal-pelvic infection.
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                                                                                                                                                                GLIFGLVYSPIVITGLHQSFPPIE-LELFNQGGSFIFATASMANIAQGAACLAVFFLAKS 173
                                                                                                                                                                                                                                                                                                                  ---LGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAP 287
                                                                                                         236
                                                                                                                                           59 LHKRLKGTADFLITPVLTLLLTGFLTFIALGPAMRWVGDVLAHGLQGL----YDFGGPVG 114
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----TDAFADILELDQKEII 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKKEAV 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKLKGLAGASGVSAVLGITEPALFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVA---
                                                                                                                                                                                                                                                                                                                                                                                                                                       288 VPAGTIKAERAPAEFSNDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGVAIVPTKGQL
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                                                                                          293 GLIMGSLWQVFVMFGMHWGFVPIMFLNIEQYGFDVLMPMLLPAILAQGGAALAVALRTKD
                                                                    1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDV - - AQAGYQGTVLFVLVVSWILATIEKF
                                    56; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae cellular proliferation protein #303.
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Length 628;
                                    Indels
   28.0%; Score 662; DB 7; L
33.5%; Pred. No. 1.4e-56;
ive 89; Mismatches 172;
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 DB 7;
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Xu HH;
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23-MAY-2000; 2000US-0206848P.
26-MAY-2000; 2000US-0207727P.
27-NOV-2000; 2000US-025362F.
22-DEC-2000; 2000US-025362F.
22-DEC-2000; 200US-025362F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae.
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                                          160; Conservative
     Query Match
Best Local Similarity
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Yamamoto RT,
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes their use in the discovery of novel antibiotics, the essential genes there leaves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, seful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous of organisms. The present sequence represents an essential prokaryotic cluster proliferation protein. Note: The sequence data for this patent of clumar proliferation protein. Note: The sequence data for this patent of electronic forms part of the printed specification, but was obtained in expense.
                                                                                              New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids.
                                                                                                                                                                       Example 3; SEQ ID NO 13467; 511pp; English.
                          WPI; 2001-611495/70
                                                 N-PSDB; AAS55733
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Sequence 627 AA;

KRLKGTADFLITPVLTLLLTGFLTFIALGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL 120 VYSPIVITGLHQSFPPIELELFNQGGSFIF-ATASMANIAQGAACLAVFFLAKSEKLKGL 179 1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH Gaps 26; Length 627; 27.9%; Score 660; DB 4; Length 62' 34.3%; Pred. No. 2.1e-56; .ive 92; Mismatches 187; Indels Query Match 27.37 Best Local Similarity 34.37 Matches 159; Conservative 61 121 à g à g δ 셤

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180 AGASGVSAVIGITEPAIFGVNIRIRNPFFIGIGTAAIGGALIALFNIKAVALGAAGFIG- 238 239 VVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAE 298 -APAEFSNDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVV 357 358 299 ò Пр à gg ò 유

AFPSGHAFAVRIKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDBVKAGELLCEFDID 417 358

AIKAAGYEVITPIVVSN---YKKIGPVNTYGLGEIEAGANLLNV 458

418

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